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From:

Rao, Manjunath N.

⊮Sent:

Wednesday, October 02, 2002 9:16 AM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search request for 09/656,640

From: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10C 01

Phone: 306-5681

Dat: 10-2-02

Please search the following as soon as possible for application with serial number 09/656,640

SEQ ID NO:1, and 3 against all commercial nucleic acid databases including issued patents database and pending application database and provide a print of all results.

SEQ ID NO:2 and **4**, against all commercial protein databases including issued patents database and pending application database and provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D. Bi technology Patent Examiner Art Unit 1652, Room 10A11 Crystal Mall 1, USPTO.

CONTED 2002

POINT OF CONTACT:
PAUL SCHULWITZ
TECHNICAL INFO. SPECIALIST
CM1 6B06 TEL. (703) 305-1954

	TYPE OF SEARCH:	VENDOR/COST (where applic.
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Stachybotrys chartarum
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota
1 (bases 1 to 1958)
Convents, D. U., Doornink, M. U., de Vries, C. H. and Wan
Detergent compositions comprising phenol oxidizing
Patent: WO 0121748-A 1 29-MAR-2001;
Location/Qualifiers
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Phenol oxidizing enzymes

Phetent: US 6168936-A 3 02-JAN-2001;

Patent: Location/Qualifiers

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NM M. verrucaria mRNA for bilirubin oxidase, con

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bilirubin oxidase.

Myrothecium verrucaria (strain:MT-1) cDNA to

Myrothecium verrucaria

Eukaryota; Fungi; Ascomycota; mitosporic Asco

1 (bases 1 to 1942)

Koikeda, S., Ando, K., Kaji, H., Inoue, T., Murae,

Koikeda, S., Ando, K., Kaji, H., Inoue, T., Murae,
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Myrothecium verrucaria an
J. Biol. Chem. 268 (25),
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2 (bases 1 to 1942)
                        Molecular cloning of the gene for bilirubin oxidase Myrothecium verrucaria and its expression in yeast J. Biol. Chem. 268 (25), 18801–18809 (1993)
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22 Miyukigaoka
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aggcccactacgctcctttcccgtaagttctcgccttttacctaactggttttcactcat
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TITLE
JOURNAL
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Best Local
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OS MYTOThecium verrucaria
PN JP 199319982-A/1
PD 10-AUG-1993
PF 24-JAN-1992 JP 1992034126
PI ANDO KEIICHI, KOIKEDA SATOSHI, SAMEJIMA TATSUYA PC C12N15/53, C12N1/19, C12N9/06, (C12N15/53, C12R1:645); CC strandedness: Double;
CC topology: Linear;
CC *source: strain=MT-1;
FH Key Location/Qualifiers
FH CDS 66. 1794
FT CDS 66. 1794
FT sig_peptide 66. 1781
FT mat_peptide 180. 1781
FT product='Bilirubin oxidase'.
                                                                                                            gttgctaatcattgcagtaccgtccccaacccccaacactggagaggacatcttgtactac 298
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                                GAGGTCGAGATCAAGCCCTTCACTCACCAGGTTTACCCTGACCTTGGATCCGCTGATCTG
                                                  gagatggagattaggcccttctcccaccagatctaccctgatctggagccggccaacatg
                                                                                             GTTAAGCAGCCCCGCTTGACTGTAACCAATCCTGTGAATGGACAAGAGATCTGGTACTAT 296
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PRODUCTION OF BILINUBIN OXIDASE

PATENT: JP 193199882-A 1 10-AUG-1993;

AMANO PHARMACEUT CO LTD

OS MYTOTHECIUM VETRUCATIA

PN JP 199319982-A/1

PD 10-AUG-1993

PF 24-JAN-1992 JP 1992034126

PF 24-JAN-1992 JP 1992034126
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Bilirubin oxidase gene
E05283
E05283.1 GI:2173473
JP 1993199882-A/1.
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1 (bases 1 to 1959)
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                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                     457
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/db_xref="taxon:5532"
549 c 436 g 517 t
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62.0%;
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Pred. No. 1.5e-114;
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreales; Hypocreaceae; mitosporic Hypocreaceae; Acremonium

1 (bases 1 to 2126)

1 (bases 1 to 2126)

Gouka, R.J., van Der Heiden, M., Swarthoff, T. and Verrips, C.T.

Cloning of a Phenol Oxidase Gene from Acremonium murorum and I

Expression in Aspergillus awamori

Appl. Environ. Microbiol. 67 (6), 2610-2616 (2001)
                                                                                                                                                                                                                       Submitted (19-JAN-2000) Gouka
Research Vlaardingen, Olivier
Vlaardingen, NETHERLANDS
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gggtgacttcagcgagcttgccatcactgaccgcattcaggagatggctagcttcaaccc
                     CCCCATGCAGGACGAGTTCCGCGCCCAAGCCGTACGTGGACAACGACGTCGAGGTGCGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Satoshi Koikeda
Tsukuba Research Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular cloning of the gene for bilirubin oxidase from Myrothecium verrucaria and its expression in yeast J. Biol. Chem. 268 (25), 18801–18809 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myrothecium verrucaria (strain:MT-1) DNA.
Myrothecium verrucaria
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.
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                                                              GRTGPTWTINGVAFADVQNRLLANVÞVGTVERWELINAGNGWTHPIHIHLVDFKVISR
TSGNNARTVMÞYESGLKDVVWLGRRETVVVEAHYAÞFÞGVYMFHCHNLIHEDHDMMAA
                                                                                                    ADTDAIDTRLPFKVIASDSGLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNL
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join(1104. 1191,1353. 1504,1564. 1955,2036.
2677. .826.2878. 3141)
/EC_number="1.3.3.5"
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caaggattactactaccccaacaggcaggctgcccgcatgctttggtaccatgaccatgc 597
                                                                ctctttctctcgagctccctttgatggttgggctgaggacactacccagcctggcgagta 537
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                                                                                                                                                        tgttgtccgcttcgtgaacagcggagagaacacctctcccaacagcgtccacttgcacgg 477
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2827. .287
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1505. .15
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1292. .1352
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2677. .2826,2878. .3138)
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                                                  atgaccatgccatgtccatcaccgccgagaacgcctacatgggtcaggctggtgtctaca, 647
                                                                                         CGGGCGGCTCGAAGGTCTACGACTACCCGAACCTTCAGCGCGGCGCGCGACGCTCTGGTACC
                                                                                                                   ACCTGCACGGCGGCACGTGCCGGCCACCAGCGACGGTCACCCGATGGACCTGATCCCGC
                                                                                                                                                                                                                 GCACGGGCCGGCCCGTGCGGATCACCTACACCAACGGGCTCGACACCCCACGCCAACGTGC
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tgatccaggacccggctgaggatgccctgaacctccccagcggctacggcgagtttgata 707
                               ACGACCACACCCCACGCCTACGAGGCCGACCACGTCTACCGCGGGACTGCACGGCTTCTATC
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HOSTAG,T.J., HOTAN,A.C. and Wang,T.X.
Everninomicin biosynthetic genes
Patent: WO 0151039-A 1 19-JUL-2001;
Schering Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Micromonospora carbonacea.
Micromonospora carbonacea
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Micromonosporineae; M
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Sequence 1 from Patent W00151639.
AX195929 AX195929.1 GI:15386161
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/db_xref="taxon:47853"
39910 c 39406 g 15102 t
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                                                                                                                                                                                                                                                                                          4.98;
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.2e-12;
les 172;
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RESULT 14
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TITLE
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Best Local Similarity
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                                                                                   gctgaggatgccctgaacctccccagcggctacggcgagtttgatatccccttg 715
                                                                                                                                 GACTACGAGGCCGACCACGTCTACCGGGGCCTGCACGGCTTCTACCTCATCGAGGACCCC
                                                                                                                                                                                                                 gattactactaccccaacaggcaggctgcccgcatgctttggtaccatgaccatgccatg
                                                                                                                                                                                                                                                                 CGCGTGCCGGCCAGCAGTGACGGGCACCCGATGGACATCATCGAGCCGGGCGGCTCGCGG
                                                                                                                                                                                                                                                                                            ttctctcgagctccctttgatggttgggctgaggacactacccagcctggcgagtacaag
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                                                                GCCGAGCGGCACCTGCACCTGCCCAAGGGGCGCTACGACGTCCCGATCCTGCTG
                                                                                                                                                                                                  GTCTACGACTACCCGAACGTCCAACGCGGGGCCACGCTGTGGTACCACGACCACACCCAC
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Sequence 4 from Patent W00155180.
AX204969
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Staffa, A., Zazopoulos, E., Mercure, S. and Nowacki, P. Genetic locus for everninomicin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: WO 0155180-A 4 02-AUG-2001
Ecopia Biosciences Inc. (CA); Far
Location/Qualifiers
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF 2 (positive strandedness) incomplete: C-terminus only (N-terminus undetermined)" 1077. 2231 /note="ORF 3 (positive strandedness)" 2242. 3444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2242. .3444
/note="ORF 4 (negative strandedness) Incomplete:
C-terminus only (N-terminus undetermined)"
a 1148 c 1315 g 556 t
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/db_xref="taxon:47853"
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55.1%;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 82.8; DB 6;
Pred. No. 5.9e-09;
0; Mismatches 132
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AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biology, Slovak Republic 84251, Slovak Republic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-MAY-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct
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Kormanec, J., Bistakova, J.,
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                                       /translation="msvvarelvaaagyrraggtsgtgpgvgagrepgdgpggqapga
vpggvagrgagergalrllsslsqvplgllafaqafavamivyprteapppqpgdhaw
whsagpvepeafrpglflalatvafyltlpllalagqvlrrrggrlvgaggrslpaql
GAPWAAAAGAPSLRRESGSLHAESS"
                       GFAAAATAVGAVVTVPLVVLARAFSPVDGGPLGAVVTADAVTAMRLCALAALLLAFVA
                                                                                                                                                                                                                                                             complement(1782.
                                                                                                                                                                                                                                                                                                              complement(1782. .2513)
                                                                                                                                                                                                                                                                                                                                  GQYLYHCHQLGHSSGGQMGRIDIVA"
                                                                                                                                                                                                                                                                                                                                                       LTTYPPQPTPTVERDFEIRTFPAMTINGQSYDPNRVDITAKLGTTEVWTVRNVEAPAA
PGKPDFHLWHSFHTHLTYFRVLERNGKPAGTRDLGLKDTVTLGPGDTVKIAMTWGPYT
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MLVNGKERPYFQVAARKYRFRVYNACANRYVKLRFADGIEFTQIGTDGGFLETPVQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="oxidoreductase-like protein"
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/db_xref="G1:1446272"
/translation="MAAAGGAAALFPWDRLTGAGSQAVASSLATAEAAPIVPFAHAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Aur21; similar to Bacillus subtilis spore-coat
protein CotA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ces aureofaciens
Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:14486270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene Expression, Institute of Molecular of Sciences, Dubravska 21, Bratislava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novakova, R.,
                                                                                                                                                                                                                                                                  2513)
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DDPGTASRPFDATRNGFVLGEGSAVLVLEDLESARKRGAHVYAEISGFASRCNAYHMT
GLRADGVEMAEAITVALDEARLDPSAVDYINAHGSGTKQNDRHETAAFKRSLGGRAYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5386.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEDTVQIEGSAKDVYDFVNEADRWHERLPHVATVRLREDTPGLQELEMDTRAKDGSVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPEGPGEER I RIWATANGEAKNWTSRRTLDAEALR I TFRQEVTAPPVAAMGGTW I I EE
LSAQESRVRLLHDYRAVDDDADSLAWI DEAVDRNSRSELAALKKNVEAAHAAEELTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="cyclase/dehydratase-like protein"
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'note="Aur2B"

'product="chain length factor-like protein"

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BASE COUNT
ORIGIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1526 TACGACGCCACCTTCCCCGGCCCGACCATCCGGGCGACCCAGGGCCGTGAGGTCGTCGTC 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                             1412 GTGCTCTCCGAGCACGACGGCCTGCCGATGGACACCATCGTGCCGGGCGGCGAACGTACG 1353
                                                                                                                                                                                                                                                 545 tactactccccaacaggcaggctgcccgcatgctttggtaccatgaccatgccatgtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 tacgatggcatgtccccaggacctaccatcatcgttcctcgtggcactgagagtgttgtc 424
                                 665 gaggatgccctgaacctccccagcggctacggcgagtttgatatccccttggttctgact 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 216; Conserv
                                                                                                                                         atcaccgccgagaacgcctacatgggtcaggctggtgtctacatgatccaggacccggct
                                                                                                                                                                                                                                                                                                                                                                                                                                       CG-----GCAGATCAACGAGCTCCAGGTGAACACCGCGGTCCACCTGCACGGGGCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgcttcgtgaacagcggagagaacacctctcccaacagcgtccacttgcacggctctttc 484
                                                                                                          CTGGAGGCCGAGAACGTCTTCATGGGCCTGCACGGCCTGTACCTGCTCACCGACCACAC
                                                                                                                                                                                                                     TACCGCTACCCGAACAACCAGCCGGCGGCGTCGCTGTGGTACCACGACCACGCGCACCAC
                                                                                                                                                                                                                                                                                                                                                              tctcgagctccctttgatggttgggctgaggacactacccagcctggcgagtacaaggat
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8524. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coelicolor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="aur2C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 81.4; DB 1;
Pred. No. 1.3e-08;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to
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-TACGACGTCCCGCTCGTCATCCGG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             actI dimerase from Streptomyces
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REFERENCE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1178
                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.
The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of p0037C04 clone has an overlap with p0445D12 (DDBJ: AP003046) clone at the position 1 to 45,349 of 5' end. The sequence of this clone starts at the position 95,604 of P0445D12. This sequence of p0037C04 clone has an overlap with p0044F08 (DDBJ: AP002909) clone at the position 48,431 to 137,879 of 3' end. The sequence of this clone ends at the position 89,449 of p0044F08. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gccaagcgatacaacgcagacggcactctcttctccacc 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGCGCGCGTCGAGGCGGACGGCACCCTGCTCTACACC 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on May 15, 2001 this sequence version replaced gi:13365490. Genes were predicted from the integrated results of the following: GENSCAN1.0, BLASTN2.0, BLASTN2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel.81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa genomic DNA, chromosome 1, PAC clone:P0037C04 AP003233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (cultivar:Nipponbare) DNA, clone:P0037C04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP003233.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plished Only in DataBase (2001) In press (bases 1 to 137879)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (sites)
/protein_id="BAB55515.1"
/db_xref="GI:14090357"
/translation="MAIWAARHGTAQARPCLGRGLSGWHGPTDAPGRAVPAHGRHTRP
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/gene="p0037C04.1"
                                                                                                                                                                                                                         join(905. .1139,1595. .1860)
/gene="P0037C04.1"
                                                                                                                                                                                                                                                                                                                                  /cultivar="Nipponbare"
/db_xref="taxon:4530"
/~hr~m~come="1"
                                                                                                  /codon_start=1
                                                                                                                         'note="hypothetical protein"
                                                                                                                                                                                                                                                                                        /clone="P0037C04"
                                                                                                                                                                                                                                                                                                                            /chromosome="1
                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137879 bp
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gene

gene

CDS

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OVEBETTKMTYSIDSDSLEACPSCNEPIGDIRCRFLEKVLAAMSAPCKFRASGCMET
VGFTERLSHEASCTHAPCGCDFDGCTYLGLLLYNHILDEHATDAVVAMGSLRGTTVTVV
HKSKPFNVLLHRGGTRGGNRVFLLLNGGDVLSGRSLSLVSVGPPPTANCELLYKIELA
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/db_xref-"GI:14090360"
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VAGGPYVEEKAASRSGYPPDPMGPPDPAVGGGGGGYRRIRIRRLPSGGEGGGGWRSA
ERTQRSGDREKREERRKREDREEERREEKRLVDEVISDEALMSITNRPSQMGRSGVV
                                                                                                                                                                                                                                                                                                                                                                                                  VLLKTRTSQDRDSSVAQKQDPTEASSDGHRDVDGAGRAPSKHPARTETIWPRTPLHAS
DARNGARYRQMIEPVHGAHLGRLLLPVAARLLPPAASSRRPPPPPPPADAALAARIV
VVVAAFSSSSRRLPSSSPLSSPTPAAELAFSLAGRRARLLSRRPRRPSSSPPLSSPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(18962. .19079,19226. .19636,19997. .20204
20474. .20575,20871. .20948,21217. .21321,21330.:(21552))
/gene="p0037C04.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGAIKFLALIGYCEEASCPANEVKLKTWSLSPDFKHWKEETTLTVGDIWASESFNQMG
LPHVLPFSPLLGVNEDGIMYAVLNHVKEEPIPRLNEFGDSLGIQLVPKANYMIRFDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HKGIVVIYAHRCYLLYDASNNHLTAIPPVPDSVFVPLGRSAVLVSAAGADDDDYILAD
IVTSCSRRGINPALPKATIFARVKNGGEWIQSSIPHLPLPPHLCGPTYFFHIDTAFSF
AGTIFWVDLLKGILICDEILSSPQGPRLVFVPLRHCIDAHDKPRHCFSPDGHRSIGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="madprpppcvllervvrfveaagltsggasrdadvaatieaggw
SwsrvQmmgsaeemerrmapsvkpvafladppqasslhmllppparttllgigei§gt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similar to Oryza sativa chromosome unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0037C04.4"
/note="cont-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(15496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB55516,1"
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LISTIYVTLYHVLREEDSRVFLLLNGGDVPKGRSLSVVCVAAAGEAELYTMAVSGGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probably inactive due to stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P0037C04.2"
complement//cr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHGPILVGPCRAGPKARWAIVLPHRKSLYLVPQLSSSSRCYRHPRLLLSKVVVDERRR
RQIHYCCRGRRPLLSSQRSSSQPAVVIWRPPPSMPRRIRGLKSPTPPPQQNPDAHLAA
                                                                                                                                                                                                                                                                                          join(25223. .25413,25596.
/gene="p0037C04.6"
                                                                                                                                                                                                                                                                                                                                                    PTNQTHEVRRMSRVAAAAEGRR"
                                                                                                                                                                                                                                                                                                                                                                         AAELSFSLAGHRARRPRRPSYPPPRSSPAPAVLSAASLASSCNQTLSKKRRPCPIRVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRLFYCFTLFOTOLTLIFVTSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNKVLSSTKISKKPTFRWFTMTFLASDFSAYLQDRQVLNLLTTATLIATHFTSLADHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB55517.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="P0037C04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(15496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALSLSASGSVPRVRRWVRYPTGGFLFVPDAYWRASGGSVSVTVHVKKLPPPELEEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(10530. .10652,12160.
/gene="P0037C04.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pseudogene, similar to gag-pol polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4956. .8529)
/gene="P0037C04.2"
/note="probably inactive due to frameshift(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="P0037C04.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(10530. .10652,12160. .12528)
/gene="P0037C04.3"
                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                           join(25223...25413,25596.
/gene="P0037C04.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="P0037C04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST C28475(C61239)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .12528)
                                                                                                                                                                                                                                                                    .26220)
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Db 131855 CTCACCCGCGCCAACCTCCTCGCCGGACTCCTCGGCGCCCTACGTCATCCGCAACCCGGCG 131914
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29; Conservative
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pfeDRYVMCKNGHAAGGSCYAKNNTMCPCLIBFIGNIRCRPLEKFVLAAMSAPGRFSTS
AYMRLIRASGCTEIVATERRNHEASCPHAPCUCPFDGCNYOGHLLYSHIQDEHATDA
AVVATGCLRGTGTTVTLHKSKPPHVLLHRGGSRVFLLLNGDNVLSGRSLSLVCISPP
ALPNCELLYKIELGAVSRAPGELGLSMSGTVPCVRRLEGFDAKAFLFVPDSYWGSSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(42298. .43077)
/gene="P0037C04.11"
/note="contains ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFVCDDWYPTINPGPVCTPRPPWKCCDNIVRLPERINPPFWQCDDELEPGQCFRQCEA
CRDPPGRPFPGRPLICDDVFWGDDPGTSCAPSSEWPWGPCCDIAVCTKSLPPICHCSD
EVESCAAACGQCEMVDSWSWRPLFVCRDSFTGDPGPRCTPEMHN*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(35545. .35965,38859. .39226))
/gene="P0037C04.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(35545...35965,38859./gene="P0037C04.10"
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QAAVEGTSLRYGMKDAVQARYTVPDDMLLRQGDAVQVFYRKATSAAGAANNN"
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/gene="P0037C04.9"
join(32915. .33391,33775.
/gene="P0037C04.9"
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/gene="p0037C04.8"
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SRWRPPVSCKLASAERQGAVAASSEPAMGQTEGRPGGGGPALGRLRRHAAGKVASRS
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AAEQAVASGEGPDGRRARRCPGGPVHARSRWRPPVSCKLASAERQGAVAASSEPAMGQ
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/gene="p0037C04.7"
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complement//^^^
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tdgnkQaksrpweccdniemsvlkiypprwrcndevkQcaaacenclQlvpgaggedv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative Bowman /protein_id="BAB55523.1" /db_xref="GI:14090365"
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PSPRSDDREDDDDEQDGSWYHPPADNEFTVRIDGIGADDGIFRCDGCFAMLSSPIYEC
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/protein_id="BAB55522.1"
/db_xref="GI:14090364"
/translation="MSSGRVCDRIAIPAAGTARRRRRDPTTGPESPVYLEGSRWSLSP
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TQSQPTVTVIEDLKLEIGKLVTSNTNR"
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/gene="P0037C04.7"
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/db_xref="GI:14090363"
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/db_xref="GI:14090362"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.18;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 79.8; DB 8; Pred. No. 3.2e-08; 0; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .34458)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .34458)
                                                                                                                                                                                                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 137879
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Search completed: October 5, 2002, 20:23:09
Job time: 8724 sec

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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM nucleic -
                                                                                                                                                                                                                            No
                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    1956.4
1956.4
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/Na2001A.DAT:*
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D)	AAK74866	22	23457	2.0	٠	44
Ś	AAX20599	20	20757		•	43
N. meningitidis pa	AAA81723	21	523	٠	38.8	42
ger pH	AAQ56945	5	2071		•	41
id	AAQ58121	15	2071	2.0	٠	40
Human immune/haema	AAK83220	22	15772	2.1	40.4	39
#8506	AAI39820	22	600	2.1	•	38
bone m	AAK34097	22	600	2.1	•	37
Human brain expres	AAK08219	22	600	2.1	٠	36
#6837 f	ABA28371	22	600	2.1	40.8	35
	ABA59948	22	600	2.1	•	34
Human skeletal mus	AAH57385	22	2012	2.1		3
	AAK83212	22	m	2.2	43.6	32
Human immune/haema	AAK67283	22	68356	2.2	43.6	31
Propionibacterium	AAS59545	23	61313	2.2	44	30
Gene encoding a su	AAA10594	21	10732	2.3	44.8	29
secreted	AAA43411	21	523	2.4	47.2	28
at secreted	AAA43363	21	523	2.4	•	27
C glutamicum codin	AAH68527	22	349980	2.5	49.6	26
٠.	AAF71220	22	1614	2.5	•	25
	AAH66018	22	1533	2.5		24
	AAA51317	21	858	4.5		23
Amerosporium atrum	AAA50022	21	858	4.5	87.4	22
CO.	AAS08693	22	109519	4.9	95.8	21
S	AAA51315	21	2905	.4	283	20
	AAA50020	21	2905	14.5	283	19
	AAA51316	21	2063	14.7	288	18
۵	AAA50021	21	2063		288	17
	AAA51313	21	3677		00	16
	AAA50018	21	3677	5	00	5
	AAZ27602	20	3677	ū	00	14
	AAZ25728	20	3676		300.4	13
tachybotrys	AAZ27609	20	2067		300.4	12
Stachybotrys chart	AAZ25735	20	2067	15.3	00.	11
Stachybotrys chart	AAZ25727	20	1791		458.8	10

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ALIGNMENTS

RESULT AAF30028 THE PROPERTY OF THE PROPERTY O exon exon CDS exon Stachybotrys chartarum pulp; paper; Phenol oxidising enzyme; phenol oxidase B; spoB gene; bleach; pulp; paper; textile; detergent; ss. Stachybotrys chartarum phenol oxidase B spoB gene 23-APR-2001 AAF30028; AAF30028 standard; DNA; 1958 BP. intron intron intron (first entry) /*tag= e 889..1628 /*tag= d 806..888 /*tag= b
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Matches 1958;
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oxidising enzymes may be used in the detergent, paper, pulp, textile and food industries. They are used for preventing the transfer of dyes in solution from one textile to animodifying detergent washing, or in modifying the colour associated with dyes and coloured compounds having different chemical structures, such as in pulp and paper bleaching, bleaching the colour of stains on fabric and in detergent and textile
                                                                            enzyme. The invention relates to detergent compositions comprising more surfactants and a phenol oxidising enzyme having at least 68%
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                                                               identity to the Stachybotrys chartarum phenol oxidising enzyme.
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DB; AAB81505.
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RESULT 4
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ID AAF30029 standard; DNA;
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2095 BP

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                                                                                                          Query Match 99.4
Best Local Similarity 99.8
Matches 1948; Conservative
                                                                                                                               The present sequence is that of the Stachybotrys chartarum MUCL 38898 spoB gene encoding phenol oxidase B (see AAB20097). The gene was isolated by PCR using primers (see AAF30030-31) based on 2 peptide fragments of the isolated enzyme. The invention provides phenol oxidising enzymes such as phenol oxidase B, or enzymes with at least 68% identity to it, nucleic acids encoding them, expression vectors, filamentous fungus and yeast host cells, and methods for the recombinant production of the phenol oxidising enzymes. The enzymes are useful for bleaching of pulp and paper, fabric stains, and in detergent and textile applications. They show optimal activity at ph 5-11, 7-10.5 or 8-10, and 20-60 or 20-40 degree C.
                                                                                                       Sequence 2095 BP; 437 A; 618 C;
                                                                                                                                                                                                                                                                                                                                 New phenol oxidizing enzyme, also useful in the detergent, paper and pulp, textile or food industries, especially in modifying the colour associated with dyes and coloured compounds, as well as in anti-dye
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                                                                                                                                                                                                                                                                                            Claim 5; Fig 3; 23pp; English.
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P-PSDB; AAB20097.
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                           gttgctaattcattgcagtaccgtccccaacccccaacactggagagggacatcttgtactac
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DB; AAR40843.
      ctgactgccaagcgatacaacgcagacggcactctcttctccaccaatggagaggtttcc
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Query Match Best Local S Matches 1041

Local Similarity nes 1041; Conserv

Conservative

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Mismatches

4e-132; ches 476;

Indels 178; Length

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Score 517.4; Pred. No. 4e-

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                     The present sequence encodes a phenol oxidizing enzyme from the fungus Acremonium murorum. The enzyme has the CBS accession number 157.72. The enzyme catalyses redox reactions and is specific for molecular oxygen as the electron acceptor. The phenol oxidising enzyme is specifically used in detergents for bleaching strains on fabrics, but also for bleaching pulp and paper and for decolourisation of plant-derived food products. The enzyme has a pH optimum in the alkaline to neutral range and can bleach a wide variety of coloured compounds, e.g. porphyrins, tannins, polyphenols, carotenoids, anthocyanins and Maillard reaction products.
Sequence
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Best Local Similarity 59.3
Matches 996; Conservative
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             1037
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10-OCT-2000 (first entry)

Stachybotrys chartarum phenol oxidising enzyme

Phenol oxidising enzyme; detergent; bleaching;

Stachybotrys

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The present sequence is that of the Stachybotrys chartarum MUCL 38898 C.DNA encoding a phenol oxidising enzyme (see AAY95537). The invention relates to detergent compositions comprising novel phenol oxidising enzymes that are encoded by nuclear acids capable of hybridising to the S. Chartarum phenol oxidising enzyme gene (see AAA50018), provided the enzymes are capable of modifying the colour associated with dyes or coloured compounds, and are produced from a bacterium, yeast or fungus (see AAY95538-40). The phenol oxidising enzymes can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. They may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidising enzyme, methods for producing the phenol oxidising enzyme, and methods for constructing expression hosts are provided.
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Best Local Similarity 59.3
Matches 996; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIL ) UNILEVER NV.
(UNIL ) UNILEVER PLC.
(HIND-) HINDUSTAN LEVER LTD
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                                                                                              This cDNA encodes Stachybotrys chartarum phenol oxidizing enzyme. Phenol oxidizing enzymes encoded by nucleic acid sequences which hybridize to this DNA are claimed, as long as the enzyme is capable of modifying the colour associated with dyes or coloured compounds. The enzymes are useful in detergent compositions and for modifying colors associated with dyes or colored compounds which occur in stains in a associated with dyes or colored compounds which occur in stains in a
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                                                                                                                                                                                                                                                                                                                                           New phenol oxidizing enzyme for modifying colors associated with or colored compounds, is obtained from fungus and is encoded by trucleic acid comprising a specific nucleotide sequence
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23-JUN-1999;
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pulp; paper bleaching; se
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Sequence
                                               sample. The enzymes are also useful for pulp and paper bleaching,
anti-dye transfer in detergent and other textile applications.
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Query Match
Best Local Sin
Matches 995;

Similarity

59

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Score 458.8; Pred. No. 5.2e 0; Mismatches

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522;

Indels Length

163; 1791

Gaps

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Conservative

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The present invention describes a detergent composition containing a purified phenol oxidising enzyme derived from Stachybotrys. The present sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The enzyme can be used to modify the colour of dyes and other coloured compounds (e.g. for use in pulp and paper bleaching also for removing stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
     Sequence
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P-PSDB; AAY45222.
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Best Local S
Matches 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a detergent composition containing a purified phenol oxidising enzyme derived from Stachybotrys. The present sequence represents a PCR fragment of Stachybotrys chartarum phenol oxidising enzyme. The enzyme can be used to modify the colour of dyes and other coloured compounds (e.g. for use in pulp and paper bleaching also for removing stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye transfer during fabric washing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Convents Wang C;
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22-DEC-1998;
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Best Local Similarity
Matches 957; Conserv
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22-DEC-1998;
22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                               This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme of the invention. The invention is used to modify a coloured compound a prevent dye transfer during fabric washing, or for stain bleaching or anti-dye transfer. It is useful in the detergent, paper and pulp, text and food industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phenol |
fabric |
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dye-transfer
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No. 2.4e-72;
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P-PSDB; AAY45222.
                                                                                                                         Convents D, Wang C;
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22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                          Stachybotrys chartarum; phenoi
detergent; anti-dye transfer;
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                                              Detergent composition containing to bleach stains and prevent dye
                                                                                                                                                              (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC
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Phenol oxidase; fabric washing; enzyme; coloured
stain bleaching; compound; dye transfer prevention; anti-dye transfer; detergent; ss.

Stachybotrys chartarum

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Best Local Similarity 55.2
Matches 957; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme of the invention. The invention is used to modify a coloured compound and prevent dye transfer during fabric washing, or for stain bleaching or anti-dye transfer. It is useful in the detergent, paper and pulp, textile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 21; Fig 6; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3677 BP; 822 A; 1056 C; 849 G; 947 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel enzyme for modifying coloured compounds used to prevent dye-transfer - \ensuremath{\mathbf{T}}
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2830	40 cctttacctaactggttttcactcacgacgacgtcacaagtggagcttacatgtggca	gb vy
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1342 2523	cggcaactgggaccccgcaaaccccactgatgacgagactttca	Оу
1282 2478	gaggtgcctgccaacctccgagatg	Qy Db
1222 2421	<pre>gataacactgacaaggtcatgcgattcg </pre>	Qу
1162 2361	cttcgctggccagtccatcgatatccgcaaccttcctg 	Оy
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The present sequence is that of the Stachybotrys chartarum MUCL 38898 phenol oxidising enzyme gene, including promoter and terminator
                                   Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition -
                                                                 WPI; 2000-514528/46.
P-PSDB; AAY95537.
                                                                                                                                  23-DEC-1998;
23-JUN-1999;
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                      Claim 1; Fig 1A-B; 45pp; English.
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sequences. The gene was isolated from genomic DNA using primers (see AAA50023-24) based on isolated peptides of the enzyme. The gene codes for a 594-amino acid protein (see AAY95537). The invention relates to detergent compositions comprising novel phenol oxidising enzymes that are encoded by nucleic acids capable of hybridising to the present DNA sequence, provided the enzymes are capable of modifying the colour associated with dyes or coloured compounds, and are produced from a bacterium, yeast or fungus (see AAY95538-40). The phenol oxidising enzymes can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. They may also be capable of modifying the colour in the absence or presence of an
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Cladosporium fulvum. Cladosporium fulvum Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et Chaetothyriomycetes incertae sedis; Mycosphaerellaceae; mitosporic M7ATIG In vitro expressed cDI Bilirubin oxidase precursor, Necrotrophic Phytophatology Research Centre Unpublished (2000) Contact: R.P.Oliver Clark,A.J., Rasmussen,S.W. and Oliver,R.P. In vitro expressed genes of Cladosporium f SABC, Perth 6150, Wei Tel: +61-8-9360-7404 Mycosphaerellaceae; Cladosporium. Email: roliver@central.murdoch.edu.au In vitro expressed genes (bases 1 to 600) +61-8-9360-6303 /organism="Cladosporium fulvum"
/strain="Race 4"
/db_xref="taxon:5499"
/clone_lib="In vitro expressed cDNAs"
/tissue_type="Mycelium"
/tissue_type="Mycelium"
/note="Vector: Lambda bluescript; A mixture of mycelial cultures grown in liquid B5 for 48 hours and transferred for 24 hours to media lacking carbon, nitrogen or supplemented with hydrogen peroxide"
a 176 c 162 g 128 t 3 others Location/Qualifiers GI:8667479 Western Australia 600 bp mRNA sequence. Cladosporium fulvum mRNA fulvum linear cDNA similar to

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1 (bases 1 to 700)

Clark, A. J., Rasmussen, S.W. and Oliver, R.P.

In vitro expressed genes of Cladosporium fulvum
                                                                                                                    Email: roliver@central.murdoch.edu.au
                                                                                                                                                      Murdoch University SABC, Perth 6150, We. Tel: +61-8-9360-7404
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Cladosporium fulvum
                                                                                                          High quality sequence POLYA-No.
                                                                                                                                                                                                       Contact: R.P.Oliver
                                                                                                                                                                                                                                                                                                                                                                                   BE187716
                                                                                                                                            Fax: +61-8-9360-6303
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/clone_lib="In vitro expressed cDNAs"
/tissue_type="Mycelium"
/note="Vector: Lambda bluescript; A m
                                                           /strain="Race 4"
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BE188099
                                                                                                              Email: roliver@central.murdoch.edu
High quality sequence stop: 664
                                                                                                                                                                                 Tel: +61-8-9360-7404
                                                                                                                                                                                                                                                                                          Unpublished
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In vitro expressed genes of Cladosporium f
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/organism="Cladosporium
/strain="Race 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCGGGCCAGAATATTACTATGTTCANCGGTC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAAGACGTGGTCATTTCCATGGGAGAGCGCT-TGAGATCATTATCGACTTTANCTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgacactctgtacatctctatggccgagcgctgggaggttgttatcgaccttctcccacctt 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgctggccagtccatcgatatccgcaaccttc 1159
                                                                                                                                                                                                                                                                                            Contact: Anderson, J.M.
Crop Production & Pest Control Research Unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST0376 Triticum aestivum Lambda
JA1_5A_A06_T3 5', mRNA sequence.
BE216983
                                                                                                                                                                                                                                              Tel:
                                                                                                                                                                                                                                                                                                                                Unpubl
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bread wheat
                                                                                                                                                                                                                                                                                                                                                                  Analysis of an EST database
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                                                                                                                                                                                        primer: T3
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 139
                                                                                                                                                                                                                            765-496-2926
                                                                                                                                                                                                                                            Lilly Hall, West Lafayette, 765-494-5565
                                                                                                                                                                        quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                              ished (2000)
                                                                                                                                                                                                          janderson@purdue.edu
                                                                                                                                                                                                                                                                                                                                              in wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: Lambda bluescript; A mixture of mycelial cultures grown in liquid B5 for 48 hours and transferred for 24 hours to media lacking carbon, nitrogen or supplemented with hydrogen peroxide" a 174 c 174 g 140 t 27 others
                /clone="JA1_5A_A06_T3"
/clone_lib="Triticum aestivum Lambda
/tissue_type="leaf"
/dev_stage="9 day old seedlings"
                                                                                     /db_xref="taxon:4565"
                                                                                                    /strain="P29"
                                                                                                                    /organism="Triticum aestivum"
                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Mycelium"
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Pred. No. 4
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                                                                                                                                                                                                                                                          IN 47907, USA
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probable
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JOURNAL COMMENT
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HY_CEA0010G19f Hordeum vulgare seedling g
HYCDNA0004 (Blumeria challenged) Hordeum
HY_CEA0010G19f, mRNA sequence.
BF264805
                                                                                                                                                                                                                                                                                                                                                                                      Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University
100 Jordan Hall, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
On Nov 17, 2000 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,D.W., Fenton,R.D., Oates,R. and Main,D. Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (MIal3) seedling leaf cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
Total hq bases = 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                          primer: AATTAACCCTCACTAAAGGG
h quality sequence stop: 798.
                                                                                                                                                                                                                                                                                       quality sequence stop: Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             University Genomics Institute
C.I. 16155 (Mla13) plants were greenhouse grown in the R Wise lab at lowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate A27 (AvrMla13) Of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen;
                                                                                                                          /db_xref=".caxu...-//db_xref=".caxu...-//clone="HY_CBa0010G19f"
/clone_lib="Hordeum vulgare seedling green
library HVcDNA0004 (Blumeria challenged)"
                                                                                                          /tissue_type="seedling green
/lab_host="TJC121"
                                                                                                                                                                                                                               /organism="Hordeum
/cultivar="CI16155
                                                                                               /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                                                                                                                                                                                                               /db_xref="taxon:45]
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55.2%;
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Pred. No. 2
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(Mla13)"
(13"
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2.7e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   757
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1 (bases 1 to 465)
                                                                                                  Department of Botany
The University of Georgia
Plant Sciences Building,
                                                  Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                   Unpublished (2000)
Contact: Cordonnier-Pratt
                                                                                                                                                                                                                                                                                           Cordonnier-Pratt, M. - M., Gingle, A., Paterson, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Sorghum propinguum
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EST.
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primer:
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  mmpratt@uga.edu
imer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      this clone see http://www.genome.clemson.edu/orders Also see close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" a 198 c 318 g 149 t
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1.6e-05;
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BASE COUNT ORIGIN

Query Match Best Local

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RESULT 6
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REFERENCE AUTHORS

SOURCE

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Lotus japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 311)
Asamizu,E., Nakamura,Y., Sato,S.
Generation of 7137 non-redundant
legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV426401 311 bp mRNA linear EST 23-AV426401 Lotus japonicus young plants (two-week old) Lotus japonicus cone MWM066f04_r 5', mRNA sequence.
AV426401 AV426401
                                                                                                                                                                                        Yana 1532-3, Kisarazu, Chiba
Email: ynakamu@kazusa.or.jp,
Location/Qualifiers
                                                                                                                                                                                                                                                           The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: POLYA=No.
                                                                                                                                                                                                                                                                                                     Contact: Yasukazu Nakamura
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a 128 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: Rhizomes; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 128 c 193 g 72 t
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhOI; isolate=Miyakojima MG-20"
100 c 68 g 62 t
                                                                                                      /clone="MWM066f04_r"
                                                                                                                            /organism="Lotus japonicus"
/db_xref="taxon:34305"
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/db_xref="taxon:132711"
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                                                                                                                                                                                                                 292-0812, Japan
URL:http://www.kazusa.or.jp/en/plant/
                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence tags from
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les 115; Conserv
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                                                                                                                                                                                                            Email: tshini@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript(KS), that.
was in vivo excised from a modified IPs phage vector (Mo bi Tec, and the part of the cDNA that was digested with Xhol was ligated to SalI site of the vector and the 3' end including polya.

tail was ligated to BamHI site of the vector. cDNA instert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al.

Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light.
                                                                                                                                                                                                                                                                                                                                                                                                                 Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 580 bp
BJ159802 full length cDNA library,
gametophores Physcomitrella patens
pph17c15 5', mRNA sequence.
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Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta;
Bryopsida; Funaridae; Funariales; Funar
1 (bases 1 to 580)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comparison of the moss
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                                                              gametophores with 2 to 138 c 170 g 1
                                                                                                                                         /organism="Physcomitrella
/db_xref="taxon:145481"
/clone="pph17c15"
                                                                                                             young gametophores"
                                                                                                                           /clone_lib="full length cDNA library,
                                                                                            /tissue_type="mixture of chloronemata
                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (2002)
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izaki,Y., Shinozaki,K.,
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Pred. No. 0.044;
0; Mismatches 106;
   Score
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 50;
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 DB
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Length
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K., Kohara,Y.
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                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen
South Memorial Parkway Huntsville, AL 35801 For furt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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Spermatophyta;
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BM143324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact:
                                                                                                                                                                                                                                                                             www.resgen.com
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    a; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    phyta; Magnoliophyta; eudicotyledons; core eudicots;
    eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae

/tissue_type="seedlings induced
(Sudden Death Syndrome) disease'
                                                      /clone="SOYBEAN CLONE ID: Gm-c1072-2563"
/clone_lib="Gm-c1072"
                                                                                                                                                                                                Location/Qualifiers
                                                                                                               /db_xref="taxon:3847"
                                                                                                                                         /organism="Glycine max"
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                                                                                                                                                                              1 (bases 1 to 766)
1 (bases 1 to 766)
Brandle, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.
                                      Contact: Jim Brandle Genomics and Biotechnology
                                                                                                                                                        Leaf ESTs from Stevia rebaudiana: diterpene synthesis
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56-88 Stevia field grown leaf cl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. Plants were inoculated by Shuxian Li (Glen Hartman lab, University of Illinois). Library was constructed by Steve Clough (Lila Vodkin lab, University of Illinois)."

university of Illinois)."
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Canada
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cDNA Stevia rebaudiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                         244 TCGTATTTG 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               accoggotgaggatgccctgaacctccccagcggctacggcgagtttgatatccccttgg 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccatgtccatcaccgccgagaacgcctacatgggtcaggctggtgtctacatgatccagg 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttctgactg 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCACGATGTCGAAGCCCCACTTGGGCTCCCTTCTGGTGATGAGTTTGATCGGCCGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATGGGGTTGACCAGGGTCAACCTTCTTGCAGGTTTGTTCGGAGCCTACATCATACGCC 183
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Al
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
                                                                                                                                                                                                                           GSS
                                                                                                                                                                                                                                                                                                     AZ714471
RPCI-24-138E2.TJ RPCI-24
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Tel: 519 457 1470
Fax: 519 457 3997
                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                          AZ714471.1
                                                                                                                                                                                                                                                                 DNA sequence.
AZ714471
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                                                                                                                                    Mammalia;
                                                                                                                                                     Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: brandleje@em.agr.ca
                                                                                                           (bases 1 to 286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Stevia field grown leaf cDNA"
/tlssue_type="leaf"
/tlssue_type="field grown, mid-size"
/dev_stage="field grown, mid-size"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBK-CMV; Site_1: ECORI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from field grown leaves. Mid-size actively growing leaves
were collected and pooled from several plants and frozen
immediately after harvesting in liquid nitrogen. The cDNA
was prepared using an XhoI-poly(dT) linker-primer. An
ECORI adapter was ligated to the blunt end cDNA and the
products were digested with ECORI and XhoI enabling
products were digested with ECORI and XhoI enabling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          directional cloning into the lambda ZAP Express vector. The library was amplified using the host strain XLI-Blue MRF'. Mass excision of the library was performed to obtain pBK-CMV phagemid clones in the host strain XLOLR. Single pass DNA sequencing was performed using the T3 promoter primer: 5'. ATTAACCCTAAAGGGA 3'. This library was constructed by Alex Richman."
                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="751/1501"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     ccggctgaggatgcc 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTTCCTCCTTAGTGGCAGGAGATGCCAAAGATAAGGACATCTCCTGGTTCTCCCCCAAT .95
                                                                                                                                                                                                                                                                                                                                                                                                                        TTTACCCTCACCATCTACAACGCCAACATCGACGATGCCGGCATATACAAGTGTGTGGTC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGAGAAGCTGAGCCCAAACCAGCAGCGGATCTCAGTGGTGTGGAATGATGACTTCTTC 155
1 (bases 1 to 599)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
,R.D., Oates,R. and Main,D.
                                                                                                                                                                                                           BF258534 599 bp mRNA linear EST 22-OCT-2001
HVSMEF0015P2lf Hordeum vulgare seedling root EST library HVcDNA0007
(Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEF0015P2lf, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                          BF258534.2 GI:13119477
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 138 row: E column: 2
                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                            BF258534
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                                                                                                                       Hordeum vulgare
                                                                                                                                           barley.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from
                                                                      Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-138E2"
/clone_lib="RPCI-24"
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52.3%;
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Query Match 2.4%;
Best Local Similarity 56.8%;
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ctgac 1071
                                                                                                           ccagacttcccttccaggtcattgccgctgacggtggtctgcttgagggccctgttgaca 1066
                                                                                                                                                                                                                                                                                                                                            AACGGCAAGGCCTGGCCGTTCCTCCGCGTGCGGCGCCGCCGCTACCGCTTCCGCATCCTC 136
                                                                                                                                                                                                                                                                    aacgctgccgtctcacgctctttcgctctgtatcttgctacct--ctgaggattcagaga 1006
                                                                       GTCGGCTCCGACTCCGTGTACCTCGCCCGGCCGGTGCCCACGGAGGGGTTCCTGCTCGCG
                                                                                                                                                                                                    AACGCCAGCAACGCGCGCTTCTTCCGCCTCTCGCGCGGCGGCCTGCGGTTTGTGCAC 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University
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Total hq bases = 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //note="Wector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 215 c 206 g 82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Hordeum vulgare seedling root EST library
HVcDNA0007 (Etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this clone see http://www.genome.clemson.edu/orders Also
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                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Fujiwake,S., Inoue,K., Togawa,X., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki,Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara, Hiramoto,K., Hori,F., Ishil,Y., Ito,M., Kawai,J., Konno,H., Ko,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Koya,S., Matsuyama,T., Miyazaki,A., Sanura,K., Sano,H., Sas,Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sas,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note-"Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory RIKEN. Division of Experimental Animal Research in Rik contributed to prepare mouse tissues. 1st strand cDNA
                                                                                                                                                                                                                                   /clone="D130015D23"
/clone_lib="RKKEN full-length enriched, 12 days embryo
spinal ganglion"
                                                                                                                                                                                                                                                                                                                                                                                                                         tissues.
                                                                                                                                                        /tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
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485 bp mRNA linear EST 21-JUL-19
uj35b06.yl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1921907 5' similar to gb:Y00051 Mouse mRNA for neural cell
                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                       Other_ESTs: uj35b06.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
.B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
.E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adhesion molecule (MOUSE);, mRNA sequence. A1876848
                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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Similarity 52.0%;
                                                                                                                                                                                                                      IMAGE Consortium (info@image.llnl.gov)
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(bases 1 to 485)
                                                                                                                                                                   primer: custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                   mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pBluescript KS(+) after bulk excision from Lambda FLC I." 180\ c 179\ g 142\ t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
/clone="IMAGE:1921907"
/clone_lib="Sugano mouse kidney mkia"
                                               /strain="C57BL"
/db_xref="taxon:10090"
                                                                                             /organism="Mus musculus"
                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer adapter of sequence [5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1.3;
0; Mismatches
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                                                                                                                                                                                                                                          royalty-free through LLNL ;
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                                                                                                                                                                                                                        for further information
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                                                                                                                                                                                                                                                                                                                                            63108,
                                                                                                                                                                                                                                          contact the
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SOURCE
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BB651243
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 CTTCCTGTGTCAAGTGGCAGGAGATGCCCAAAGATAAGGACATCTCCTGGTTCTCCCCCAA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cccggctgaggatgcc 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctctttctctcgagctccctttgatggttgggctgaggacactacccagcctggcgagta 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catgtccatcaccgccgagaacgcctacatgggtcaggctggtgtctacatgatccagga 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caaggattactactaccccaacaggcaggctgcccgcatgctttggtaccatgaccatgc 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACGGCTGAGGACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCTACCCTCACCATCTACAACGCCAACATCGACGATGCCGGCATATACAAGTGTGTGGT 444
                                                                                                                                                                                       Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 562)
1 (bases 1, Konda, Kondo, H., Kouda, M., Koya, S., Matsuyama, T., Mayazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., D., Shibata, K., Shinagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
1 (bases 1 to 562)
1 (bases 1 to
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus cDNA clone C23
BB651243
BB651243.1 GI:16485497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB651243 SIKEN full-length enriched, 0 day neonate cerebellum Mus musculus cDNA clone C230070H21 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
                                                                                                                                                                              1-7-22 Suehiro-cho, Tsurumi-ku,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                         Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nouse mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII. (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was contracted to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="female"
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
         Hayatsu, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
Sugahara,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94;
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    Shibata, K.,
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                                                                                                                                                                                                                                                                303
                                                                                                                                                                                                                                                                                                        478 ctctttctctcgagctccctttgatggttgggctgaggacactacccagcctggcgagta 537
                                                                                                                                                                                                                                                                                                                                                                                  Local
cccggctgaggatgcc 673
                                                                                                                                                                 TGGGGAGAAGCTGAGCCCAAACCAGCAGCGGATCTCAGTGGTGTGGAATGATGACGACTC
                                                                                                                                                                                                                                                             CTTCCTGTGTCAAGTGGCAGGAGATGCCCAAAGATAAGGACATCTCCTGGTTCTCCCCCCAA 362
                                                                        catgtccatcaccgccgagaacgcctacatgggtcaggctggtgtctacatgatccagga 657
                                                                                                                                                                                                                                                                                                                                                              al Similarity
102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawatahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Genome Sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with fuman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerebellum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="C230070H21
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="cerebellum"
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/clone="c230070H21"
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Search completed: October 5, 2002, 18:54:14 Job time: 3504 sec

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US-08-769-819-2
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ALIGNMENTS

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APPLICANT: Wang, Huaming
TITLE OF INVENTION: No. 6168936el Phenol Ox
FILE REFERENCE: GC584
CURRENT APPLICATION NUMBER: US/09/401,476
CURRENT FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 8
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1958
TYPE: DNA
ORGANISM: Stachybotrys chararum
US-09-401-476-1
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DB 4;

Length 1958;

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Sequence 3, Application US/09401476
Patent No. 6168936
GENERAL INFORMATION:
APPLICANT: Wang, Huaming
TITLE OF INVENTION: No. 6168936el Phenol Ox
FILE REFERENCE: GC584
CURRENT APPLICATION NUMBER: US/09/401,476
CURRENT FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2095
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite :
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 23313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)683-4109
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                 ADDRESSEE:
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                                                                 Turunen, Marja K.
Pagerstr m. Richard B.
VENTION: Production of Phytase Degrading Enzymes
                                                                                                              Rambosek, John A.
                                                                                                                                Piddington, Christopher S.
                                                                                                                                                                         Paloheimo, Marja T.
Miettinen-Oinonen, Arja S.K.
                                                                                                                                             Cantrell, Michael
                                                                                                                                                             Torkkeli,
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                                                                                                                                                                                                   Wevalainen, Helena K.M.
                Sterne,
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 New York Avenue,
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Kessler, Goldstein &
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US/07/923,77
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                                                                  684 CGGTGAGGGTTTCTTTGGCTACAACTACTCCACCAACGCTGCCCTCAACATCATCTCCGA
                                                                                                                                  624 GACGGTCGTGCCCTTCTTTCTAGTGGCTACGGACGTGTCATCGAGACGGCCCGCAAGTT 683
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 744 GTCCG
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CLASSIFICATION:
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                                                                                                                                                            ccgcatgctttggtaccatgaccatgccatgtccatcaccgccgagaacgcctacatggg 630
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RESULT 5 US-08-609-426A-1

Sequence 1, Application US/08609426A

INFORMATION:

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US-08-609-426A-1
                                                                                                                                Matches 139;
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Best Local Similarity
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APPLICANT:
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APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
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FILING DATE: 19-MAR-
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                  451 ctctcccaacagcgtccacttgcacggctctttctctccgagctccctttgatggttgggc 510
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                                                             444 CAGCATCAACACTACTGAATACAAGGGCGACCTGGCCTTCCTGAACGACTGGACCTACTA.503
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CGTCCCTAATGAGTGCTACTACAACGCCGAGACCACCAGCGGCCCCTACGCCGGTTTGCT 563
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                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                              2071 base pairs
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Turunen, Marja K.
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Cantrell, Michael
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Paloheimo, Marja T.
Miettinen-Oinonen, Arja S.K.
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30-APR-1986
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29-APR-1987
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19-MAR-1990
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Production of Phytase Degrading Enzymes in Trichoderma
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Pred. No. 0.12;
0; Mismatches 166;
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                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION UMBER: 41,264
REFERENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
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                                                                                    TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
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APPLICATION NUMBER: 1
FILING DATE: 27-JUL--
CLASSIFICATION: 435
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                                                                      SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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ZIP: 20005
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TOPOLOGY:
             STRANDEDNESS:
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             nucleic acid
DEDNESS: both
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CANTRELL, MICHAEL A.
VENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
VENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
VENTION: ENZYMES IN DESIRED RATIOS
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linear
                                                                                                                              202-371-2600
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US-08-374-652C-3

NAME/KEY:

join(136..915, 970..1089, 1142..1245, 1305..1737)

MOLECULE TYPE: FEATURE:

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Matches
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Best Local Similarity
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Patent No. 6258558
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                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or
-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1997-0: EARLIER APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Liu, Rihe
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                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                               FEATURE
1476 tcaccctgttcacattcacctcgttgacttccgagtcctttctcgttccactgcccgtgg 1535
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/007,005B FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/035,963
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139; Conser
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                                      Conservative
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                                  pred. No. 0.13;
93; Mismatches
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Pred. No. 0.12
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; LOCATION: (1)...(289)
; OTHER INFORMATION: n =
US-09-244-796-17
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LENGTH: 289
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Best Local Similarity
Matches 10; Conserv
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EARLIER APPLICATION NUMBER: 60/035, 963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064, 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
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EARLIER APPLICATION NUMBER: 09/007,005
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                                   1656 ttttcactcatgctaacatctaca
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RESULT 9 US-08-528-199-2

APPLICANT:

KUBOTA, Michio

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RESULT 10
US-08-528-199-5
; Sequence 5, Application US/08528199
; Patent No. 5763228
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Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                           1880 cactgaccgcattcaggagatggctagcttcaacccctacgcccaggctgatgatg 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                              318 GAACCACGAGTGACGCGCACCCGTGGTTCCAGGCCTCCCGCAGCGATCCCGACG 373
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FILING DATE: 14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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419 Seventh Street, N.W.,
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Pred. No. 1
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RESULT 11
US-08-966-316-10/c
; Sequence 10, Application U.; Patent No. 5932445
; GENERAL INFORMATION:
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Best Local S
Matches 88
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INFORMATION FOR SEQ ID NO:
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ADDRESSEE: BROWDY AND NEIMARK
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LOCATION:
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CLASSIFICATION:
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REGISTRATION NUMBER: :
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                                                                                                                           GAACCACACGAGTGACGCGCACCCGTGGTTCCAGGCCTCCCGCAGCGATCCCGACG 373
                                                                                                                                                                                              CCACGCCTTCCTCGACGGCGCGCACGAGCGCGGGATCCGGGTGATCATCGACTTCGTCAT 317
                                                                                                                                                                                                                 ccgccccttcctcctcggagagttcgagaatggctcgggtgacttcagcgagcttgccat 1879
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SUGIMOTO, Toshiyuki
VENTION: RECONDINANT ENZYME FOR CONVERTING
VENTION: MALTOSE INTO TREHALOSE
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Pred. No. 1.8;
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APPLICANT:

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                               Sequence 7, Application US/08286870A Patent No. 6063605
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Best Local Similarity
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TOPOLOGY: 1111C.
IMMEDIATE SOURCE:
LIBRARY: SKINBIT'
TOWE: 1869688
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Wi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: Herewith
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LENGTH: 1637 base pairs
TYPE: nucleic acid
CTDANDEDNECC: (52)
APPLICANT:
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CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                          873 AGTGACGGCGCCCTCATGGATAGACTCCTTGCAGAGTCCAAAGTCGGTCAGTTTGATGTG 814
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                                                                                                                                                                        740 gcagacggcactctcttctccaccaatggagaggtttccagc 781
                                                                                                                                                                                                                                               680 ctccccagcggctacggcgagtttgatatccccttggttctgactgccaagcgatacaac 739
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CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                              aggeaggetgeeegeatgetttggtaceatgaceatgeeatgteeatcacegeegagaae 619
                                                                                                                                        GAAGATGCCCTCTCGCTCCAGATGCGTGAAGAGCTCGCCACC 652
                                                                                                                                                                                                             GTGGAGATGGCCCAGGGCCAGCGTGATCTCAGCCAGGTAGAAGCAGGCCGTATCTTCCAG 694
              INFORMATION:
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Murry, Lynn E.
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47.3%;
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Pred. No. 2.3;
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Best Local Simu
Thes 90;
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LENGTH: 2159 base pairs
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REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: GB 8:
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNMEER: US/08/286,870A FILING DATE: 05-AUG-1994
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MEDIUM TYPE: Floppy disk
                                                                                                                                   1230 CCTGACCCAGCCCGTGAACGGCGTGCCCCGCGTGGACTTTCACTGGAAGTTCGTGACCCA 1289
1350 GG 1351
                                                                1290 CCCGATCGCCAGCGACAACTTCTACTACCCCGGCTACGCTGGCATTGGCACCCCAACTCCA 1349
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PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                           652 ccaggaccoggctgaggatgccctgaacctccccagcggctacggcgagtttgatatccc 711
                                                                                                                                                                                                                                    592 ccatgccatgtccatcaccgccgagaacgcctacatgggtcaggctggtgtctacatgat 651
                                                                                                 712 cttggttctgactgccaagcgatacaacgcagacggcactctcttctccaccaatggaga 771
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Pred. No. 2.7;
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RESULT 13 US-08-446-922-5/c ; Sequence 5, Application US/08446922

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                                                                                                                                                                                                                                                                                                                                                                                               1354 gctaatggacagtggacaatcaacggagttaccttctcggatgtcgagaaccgtctgctc.1413
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1474 actcaccctgttcacattcacctcgttgacttccgagtcctttctcgttccactgcccgt 1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: USSN 08/107,353
FILING DATE: 08-13-93
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MEDIUM TYPE: Floppy
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HYPOTHETICAL:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICANT: Srinivasan, Subha
                                                                     594 ACTGCTGGGCTTCAGCCAGAGGCCGACGATGAATGGGCGGTTGACTCGAAGGCTCCCGATT 535
                                                                                                                                                                                                      654 CTCGCAAAGCTGGGAAGAACTGTGGGTATTTGCCGCCTTGAGTAAGATTCTCTCAGATCC 595
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OPERATING SYSTEM: Apple OPERATING SYSTEM: Apple OPERATION OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
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Pred. No. 2.3;
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RESULT 14
US-08-249-189-1/c
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US-08-249-189-1
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Patent No. 5961974
                                                                                                      HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                        NFORMATION FOR SEQ ID NO:
                                             FEATURE:
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
                                                                           IMMEDIATE SOURCE
                                                                                                                                                      MOLECULE TYPE:
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STREET: 51
STREET: SEATTLE
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                                                            CLONE:
                                                                                            ORGANISM:
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CLASSIFICATION:
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                            NAME/KEY:
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N: 514
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Best Local Similarity 43.6%;
Matches 153; Conservative
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                                                PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

07/805,723
                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 07/969,703
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MCGREW, C
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
                     CLASSIFICATION:
                                     FILING DATE:
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APPLICATION DATA
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MCGREW, JEFFERY
VENTION: NOVEL CYTOKINE THAT BINDS CD40
EQUENCES: 26
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                                                                                                                                                                                     June 07,
                                     December 5,
                                                                                                             October 23, 1992
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                                       1991
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pred. No. 2.3;
0; Mismatches 198;
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Best Local Similarity
Matches 153; Conserv
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HYPOTHETICAL: N
ANTI-SENSE: NO
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                      1594 gttgtctatgttgaggcccactacgctcctttcccgtaagttctcgccttt 1644
                                                                                          1474 actcaccctgttcacattcacctcgttgacttccgagtcctttctcgttccactgcccgt 1533
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ORGANISM: MOUSE
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474
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                                                                    534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/783,707 FILING DATE: October 25, 1991
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TTTCCCATTTTCAAGCATTACCAAGTTGCTTTTCATGGTATAATATCCTTT 424
                                                                    AGAGCAGAAGGTGACTTGAGTGTAGACATAATAGAGTCCTTCTTTTTAACCGTCAGCTG
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nucleic acid
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: gb_ba:
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KEYWORDS
SOURCE
ORGANISM
                                         REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
ORIGIN
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DEFINITION
ACCESSION
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AR122997
                                                                                                                                           VERSION
                                source
                           Phenol oxidizing enzymes
Patent: US 6168936-A 3 02-JAN-2001;
Location/Qualifiers
1. 2095
                                                                          Wang, H.
                                                                                                            Unknown.
                                                                                                                                                      AR122997 2095 bp
Sequence 3 from patent US 6168936.
AR122997
                                                                                    Unclassified.

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        /organism="unknown"
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Result No.

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Description

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SUMMARIES

Matches 2095; Conservative

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Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.

1 (bases 1 to 2095)
Convents,DU., boornink,M.U., de Vries,C.H. and Wang,H.
Detergent compositions comprising phenol oxidizing enzymes
Patent: WO 0121748-A 3 29-MAR-2001;
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Stachybotrys chartarum
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1 (bases 1 to 1958)
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Patent: WO 0121748-A 1 29-MAR-2001;
Location/Qualifiers
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Ltd., Tsukuba Research Laboratories: 22 Miyukigaoka, Tsukuba,
Ibaragi 305, Japan (Tel:0298-56-5026, Fax:0298-56-5012)
On Feb 26, 1994 this sequence version replaced gi:436235.
Submitted (07-JUL-1992) to DDBJ by:
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J. Biol. Chem. 268 (25), 18801
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COMMENT:	KEYWO SOURC ORG ORG REFER AUT TIT	RESUI E0521 LOCUI DEFII ACCEI	Ъ	Qy	dp Qy	Db Qy	da l	Oy Db	0у .	Оу	Qy	ОУ	Qy	Qy db	Qу
ENT.	OURCE OURCE ORGANISM EFERENCE AUTHORS TITLE JOURNAL	RESULT 8 E05283 LOCUS DEFINITION ACCESSION VERSION	1754	971	1911 1694	1851 1634	574	1529 1791	731	1671 1507	1611 1450	1390	1500 1330	1440 1270	1380 1228
yrothecium vei 193199882-1 -AUG-1993 1-JAN-1992 JP NUO KEIICHI, 1 V53,C12NI/19,0 edness: Double poology: Linea source: strain sy	193199882-A/ rothecium verr rothecium verr rothecium verr karyota; Fungi (bases 1 to 1 (bases 1 to 1 0 DUCTION OF BI tent: JP 1931 ANO PHARMACEUT	5283 Lirubin oxid 5283 5283 1 GI:2	GCCGCAGCTGAC	ttcaaccctacgcccaggctgatga 1997	gaatggctcgggtgacttcagcgagcttgccatcactgaccgcattcaggagatggctag 1970	9ttcattgacccatggagcctctctggaggccccgcccttcctcctcggagagttcga 1910 	ATGATGGCTGCCTTTAACGCCACCGTCCTGCCAGATTATGGCTATAATGCCACTGT 163		tacatyttycactyccacaacctyatccacyayyacca 179	aggeceactaegeteettteeegtaagttetegeettttaeetaactggtttteaeteat 1730 AGCTTATTACGCCCTTTCCC	atgaggctgctggtctcaaggatgttgtctggctggctcgtcgtgaggttgtctatgttg 1670	togttgacttccgagtcctttctcgttccactgcccgtggagtcgagcctt 1610	ttgagatctggcgacttgagaacaactccaaccggttggactcaccctgttcacattcacc 1559	acggagttaccttctcggatgtcgagaaccgtctgctccgcaatgtgccccgcgacactg 1499	atgacg

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acatctctatggccgagcctgggaggttgttatcgacttctccaccttcgctggccagt
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REFERENCE AUTHORS TITLE

oxidase; ppoA gene.
Acremonium murorum.
Acremonium murorum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomyce
Hypocreacles; Hypocreaceae; mitosporic Hypocreaceae; Acremo
1 (bases 1 to 2126)
Gouka,R.J., van Der Heiden,M., Swarthoff,T. and Verrips,C.
Cloning of a Phenol Oxidase Gene from Acremonium murorum a

ycotina; Sordariomycetes; Hypocreaceae; Acremonium

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Acremonium murorum AJ271104 AJ271104.1 GI:6996277

mRNA

2126 for §

polyphenol đđ

oxidase linear (ppoA

gene) PLN 08-JUN-2001

mRNA

AMU271104

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ATACAGACCTTACGCCGCAGCTGACGA
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                                   tccccaggacctaccatcatcgttcctcgtggcactgagagtgttgtccgcttcgtgaac 500
                    TCGCCCGGTCCTACCTTCATCCAGGAGAAGGGCAGGGAGAGCGTCGTCCGCTTCGTGAAC
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Research Vlaardingen, Olivier
Vlaardingen, NETHERLANDS
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Appl. Environ. Microbiol. 67 (6), 2610-2616
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/product="polyphenol oxidase"
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/sub_species="murorum"
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                                                                                                                                                                                                                        Satoshi Koikeda
Tsukuba Research Laboratories
Amano Pharmaceutical Co., Ltd.
                                                                                                                                                                                                                                                                               Submitted (20-JAN-1993) Satoshi Koikeda, Amano Pharmaceutical Co., Ltd., Tsukuba Research Laboratories; 22 Miyukigaoka, Tsukuba, Lbaragi 305, Japan (Tel:0298-56-5026, Fax:0298-56-5012) Submitted (20-JAN-1993) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myrothecium verrucaria (strain:MT-1) DNA.
Myrothecium verrucaria
Myrothecium verrucaria
Eukaryota; Fungi, Ascomycota; mitosporic Ascomycota; Myrothecium.
1 (bases 1 to 3241)
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Direct Submission
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1011. .1291
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2677. .2826,2878. .3141)
/EC_number="1.3.3.5"
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join(1104. .1291,1353. 1504,1564. .1955,2036.
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                                                                                                                                                                                                                                           AX195966
Sequence 38
AX195966
AX195966.1
                                                                                        Hosted, T.J., Horan, A.C. and Wang, T.X Everninomicin biosynthetic genes Patent: WO 0151639-A 38 19-JUL-2001;
                                                                                                                                                                                Micromonospora carbonacea
Bacteria; Firmicutes; Actinobacteria;
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                                                                             Schering
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                                                                                                                                                                    Actinomycetales; Micromonosporineae;
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                                                                             Corporation
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/organism="Micromonospora carbonacea"
/db_xref="taxon:47853"
1. .>1422
                                                        Corporation (US)
Location/Qualifiers
                                               1. .1422
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                                                                                                                                                                    Micromonosporaceae;
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BASE COUNT
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TITLE
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SOURCE
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AX195929
    BASE
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                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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Best Local;
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Local, Similarity 54.88;
hes 2,12; Conservation
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                                                                                                   Hosted, T.J., Horan, A.C. and Wang, T.X. Everninomicin biosynthetic genes Everninom to 0.151639-A 1 19-UUL-2001, Schering Corporation (US)
                                                                                                                                                                                                                                                 Micromonospora carbonacea
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Sequence 1 from Patent
AX195929
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RPVRITYTNGLDTHANVHLHGGHVPATSDGHPMDLIPPGGSKVYDYPNLQRGATLWYH
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3 575 c 431 g 197
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DDRVTILANGKAQPYFEVAPRRYRFRLLNAALKHVFRLNLGGEPLTRIATDGGLLPAP
TSHTELALSSGERVEIVIDFAEHAGGGPVYLYDGDNPILRFDVSSRAVTDPSRVPVTL
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/organism="Micromonospora carbonacea"
/db_xref="taxon:47853"
39910 c 39406 g 15102 t
                                                                                    Location/Qualifiers
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Pred. No. 1.3e-12;
0; Mismatches 172;
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t W00151639.
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REFERENCE
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AX204969/c
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JOURNAL
Best Local Similarity Matches 162; Conserv
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Best Local Similarity
Matches 212; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Micromonospora carbonacea
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micromonosporineae; Micromonosporaceae;
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Sequence 4 from Patent WO0155180
AX204969
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Conservative
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/note="ORF 4 (negative strandedness) Incomplete:
C-terminus only (N-terminus undetermined)"
1148 c 1315 g 556 t
                                                                                                                                                                                                    C-terminus only (N-terminus undetermined) 1077. . 2231
                                                                                                                                                                                 /note="ORF 3 (positive strandedness)"
                                                                                                                                                                                                                                                                        /organism="Micromonospora carbonacea"
/db_xref="taxon:47853"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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54.8%;
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                   4.0%;
55.1%;
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                   Score 82.8; DB 6; Pred. No. 2.1e-09;
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 Mismatches
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                                    Length 3446;
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	similar to Bacillus subtilis spore- 1 	
	/translation="IYTTFRYAPLHKVPTYGTPDTRLPSSDWVSDRTLCLPLHPGLSD ADVLTVAASLIKKAVEARTAEKNARS" gene complement(3451772) CDS /gene="aur21" CDS /gene="aur21" CDS /gene="aur21"	
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	O H	
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	Qy 606 gattactacccaacaggcaggctgcccgcatgctttggtaccatgaccatgccatg 665	· <u>-</u> <u>-</u>
 -	486 gtccgcttcgtgaacagcggagagaacacctctcccaacagcgtccacttgcacggctct	
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MLVNGKERPYFGVARKYRFRVINACARRYVKLERADGLEFTQJGGFLETPVQQS
ELLMLGGERADIVVDFSRYKVGDSVVLLENPGAQSIERPEVMRFDIVRTADDYSEVPGR
ELLTYPPQPTPTVERDFEIRTFEAMTINGQSYDPNRVDITAKLGTTEVMTVRNVEAPAA
PGKPDPHLMHSEHTHLIYFRYLERNGKPAGTRDLGLKDTVTLGPGDTVKIAMTMGPYT
AKIPLGRYSTPEEVAGLVGYLASDAAASITSQALNVCGGLGNF" 5386. .6657
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AVSETLAQEVAGFGVKVTLVEAGEFRTDWSAGSMVRATPKFAYDEVLAKRRHGLSGAY
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/gene="aur2G"
complement(2510. .3367)
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/gene="aur2E"
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/db_xref="GI:14486275"
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/gene="aur2F"
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TDFPAESGP"
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RQINELQVNTAVHLHGAHVLSEHDGLPMDTIVPGGERTYRYPNNQPAASLMYHDHAHH
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/note="Aur2H"
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GAEPGHLLDISELFSEMVDFHGGLPSCAA"

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8524. .9441
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TLGSAVGCTTGLDVEYNAVSRGGSTWQDHTLAVPHLEDYFVSSMAAEVAWFVNAQG
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VWLPERRVLFAGDIVMSGATPFCLTGSISGSLAVIEKLRALGPRTIVSGHGPVGGTEL
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GLRADGVEMAEAITVALDEARLDPSAYDYINAHGSGTKQNDRHETAAFKRSLGQRAYE
VPVSSIKSMIGHSLGAIGSSKVAASALAIEYNTVPPTANLHTPDPLCDLDYTPLTARE
                                                                                                                                                                                                                                                                                                /translation="MTERSPSVAQLQEVAEDVYAYIQPDGGWCLNNAGLITAGGRPAL
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/note="Aur2D"
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LDPPLVLVCPAKTASCHDAFVTGDRFLVNVLAAEHADIASSFARSGHDKFTGSPMEPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="aur2C"
/note="Aur2C; similar to actI dimerase from Streptomyces
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7997. .8500
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                      3.9%;
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Score 81.4; DB 1;
Pred. No. 4.8e-09;
0; Mismatches 171;
                                                     Length 9531;
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JOURNAL
REFERENCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1178 GACGCGCGCGTCGAGGCGGACGGCACCCTGCTCTACACC 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1292 CTGGAGGCCGAGAACGTCTTCATGGGCCTGCACGGCCTGTACCTGCTCACCGACCACAAC 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 tacgatggcatgtccccaggacctaccatcatcgttcctcgtggcactgagagtgttgtc 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                789
(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI MonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTW 2.0 with the corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0037C04 clone has an overlap with P0445D12 (DDBJ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgcttcgtgaacagcggagagaacacctctcccaacagcgtccacttgcacggctctttc 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gccaagcgatacaacgcagacggcactctcttctccacc 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGCGCACGCTGCCGTTGCCGAGCGGTCCC-----TACGACGTCCCGCTCGTCATCCGG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGCTCTCCGAGCACGACGGCCTGCCGATGGACACCATCGTGCCGGGCGGCGAACGTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gaggatgccctgaacctccccagcggctacggcgagtttgatatcccctttggttctgact 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACCGCTACCCGAACAACCAGCCGGCGGCGTCGCTGTGGTACCACGACCACGACCACCAC 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atcaccgccgagaacgcctacatgggtcaggctggtgtctacatgatccaggacccggct 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tactactaccccaacaggcaggctgcccgcatgctttggtaccatgaccatgcccatgtcc 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tctcgagctccctttgatggttgggctgaggacactacccagcctggcgagtacaaggat 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACGACGGCACCTTCCCCGGCCCGACCATCCGGGCGACCCAGGGCCGTGAGGTCGTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                               Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp/, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On May 15, 2001 this sequence version replaced gi:13365490. Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTNZ.0, BLASTNZ.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (cultivar:Nipponbare) DNA, Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa genomic DNA, chromosome {\tt AP003233}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-FEB-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone: P0037C04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AP003233.3 GI:14090356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 137879)
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ne 1,
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP003046) clone at the position 1 to 45,349 of 5' end. The sequence of this clone starts at the position 95,604 of P0445D12. This sequence of P003704 clone has an overlap with P0044F08 (DDBJ: AP002909) clone at the position 48,431 to 137,879 of 3' end. The sequence of this clone ends at the position 89,449 of P0044F08.
                                                                                                             complement(join(18962..19079,19226..19636,19997..20204,
20474..20575,20871..20948,21217..21321,21330..21552))
/gene="p0037C04.5"
                                                                                                                                                                                                                                                       I WEGIVUI YAHRCYLLXDASNNHLTA I PPVPDSVFVPLGRSAVLVSAAGADDDDY I LAD
I VTSCSRRJ IVPALPKAT I FARVKNGGSWI OSSI PHLPLPPHLGPTYFFHIDTAFSF
AGTI FWVDLKGILI OSEILSSPOGPRLVFVFLRHCIDAHDKPRHCFSP. JHRSIGRV
SGAI KFLALI OYCEBASC PANEVKLKTWSLS PDFKHKKEETTLTVGDIWASSSROMG
SHHVELSPOT OKTONED SIM YAVLNHVKEEP I PRLNEFGDSLGI QLVFKANYMI RFDML
LHHVLFFF PLLGVNEDGIMY AVLNHVKEEP I PRLNEFGDSLGI QLVFKANYMI RFDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAB5516.1"
/db_xref="G1:14090358"
/db_xref="G1:14090358"
/translation="MODIPHHEERLLDYREEKSRDGQDKLPMGVEQSMATDKNTKPNN
LISTIYVTLYHVLREEDSRVFLLLNGGDVPKGRSLSVVCVAAAGEAELYTMAVSGGAP
GALSLSASGSVPRVRRWVRYPTGGFLFVPDAYWRASGGSVSVTVHVKKLPPPELEEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"probably inactive due to frameshift(s) probably inactive due to stop codon(s) in CDS pseudogene, similar to gag-pol polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4956. .8529)
/gene="P0037C04.2"
                                                   complement(join(18962. 19079,19226. 19636,19997. 20204
20474. 20575,20871. 20948,21217. 21321,21330. 21552))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similar to Oryza sativa chromosome 1,P0698A04.16
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(15496. .16914)
/gene="P0037C04.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="maiwaarhgtaqarpclgrglsgwhgptdapgravpähägrhyrp
mhgpilvgpcragekarwaivlphrkslylvpqlssssrcyrhprlllskvvvvderrr
ROIHYCCRGRRPLLSSQRSSSQPavviwrpppsmprrirglksptpppqqnpdähijaa
                                                                                                                                                                                                      NRLFYCFTLFQTQLTLIFVTSS"
                                                                                                                                                                                                                              QNKVLSSTKISKKPTFRWFTMTFLASDFSAYLQDRQVLNLLTTATLIATÄFTSLÅDHP
                                                                                                                                                                                                                                                                                                                                                                                                      {	t SWSRVQMMGSAEEMERRMAPSVKPVAFLADPPQASSLHMLLPPPARTTLLGIGEISGT}
                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB55517.1"
/db_xref="GI:14090359"
/translation="MADPRPPPCVLLERVVREVEAAGLTSGGASRDADVAATIEAGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="P0037C04.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0037C04.2"
complement//cr/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Join(10530. .10652,12160. .12528)
/gene="P0037C04.3"
/note="hypothetical protein"
                              'gene="P0037C04.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="contains EST C28475(C61239)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         poin(10530. .10652,12160. .12528)
/gene="P0037C04.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB55515.1"
/db_xref="GI:14090357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(905. .1139,1595. .1860)
/gene="P0037C04.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(905. .1139,1595. .1860)
/gene="P0037C04.1"
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/db_xref="taxon:4530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Oryza sativa"
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                                                                                  CDS
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/gene="p0037004.9"

join(32915. .33301,33775. .34458)

/gene="p0037004.9"
                                                                                                       PTILKADDGRIFHLSCTRERGGGGGTAMSMVCIRPDHVAGAEEEFTYEVETACORLOM
QAAVEGTSLRYGMKDAVQARVEVEDDMLLRQGDAVQVEVEKATSAAGAANNN"
complement(join(35545. .35965,38859. .39226))
                                                                                                                                                                                                       /translation="MSSGRVGDRIAIPAAGTARRRRDPTTGPESPVYLEGSRWSLSPAYQBSRRRRHDEEGYSRKRGRSRSNSPRRRRRPRSCESSRCCHTRAYQBSRRRRHDEEGYSRKRGRSRSNSPRRRRRPRSCESSFCHTREPSPRSDDREDDDEQDSWYHPPADNEFTVRIDGIGADDGIFRCDGCFAMLSSPIYE ANGDVICERCSYDDGGARVCRKGGTMELARSRAIGHLLRCIRFACKNRKYGCPSFLPRQMDDEHELSCDHEPCFCPIRRCGFAGAADSLARHLTARHGWGRLRVAYGEAAVVPVQS
                                 complement(join(35545.
                                                                      complement(join(35545.
/gene="P0037C04.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(30803. .31498,31608. .31763))
/gene="p0037C04.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(30803. .31498,31608.
/gene="p0037C04.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mwwlelrqanrrgrraaaeQavasgegpdgrrarrcpggpvhar
srwrppvscklasaerqgavaassepamgqtegrpgggggpalqrlrrhaagkvasrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(27855..28310,29207..29638,29878..29901))
/gene="p0037C04.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(27855. .28310,29207.
/gene="P0037C04.7"
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HKSKPFNVLLHRGGTRGGNRVFLLLNGGDVLSGRSLSLVSVGPPPTANCELLYKIELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:14090361"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MVAALVGEGDVEDADTNGWGWRRRPPYLRGGGRQGGGYRRPPDPVAGGPYVEEKAASRSGYPPDPMGPPDPAVGGGGGGYRRIRIRRLPSGGEGGGGWRSAETQRSGDREKREERRKREDREEERREEKRLVDEVISDEALWSITNRPSQMGRGGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLPNCELLYKIELGAVSRAPGELGLSMSGTVPCVRRLEGFDAKAFLFVPDSYWGSSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVVATGCLRGTGTTVTLHKSKPFHVLLHRGGSRVFLLLNGDNVLSGRSLSLVCISPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFEDRYYMCKNGHAACGSCYAKMNTMCPCCIEPIGNIRCRPLEKVLAAMSAPCRESTS
AYMRLIRASGCTEIVAYTERRNHEASCPHAPCVCPFDGCNYQGHLLYSHIQDEHATDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TQSQPTVTVIEDLKLEIGKLVTSNTNR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAEQAVASGEGPDGRRARRCPGGPVHARSRWRPPVSCKLASAERQGAVAASSEPAMGQ
TEGRPGGGGGPALQRLRRHAAGKVASRSLARCREGARRRGRQAAGQRHSGRQGSNEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAELSFSLAGHRARRPRRPSYPPPRSSPAPAVLSAASLASSCNQTLSKKRRPCPIRVY
PTNQTHEVRRMSRVAAAAEGRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAB55521.1"
/db_xref="GI:14090363"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADGPGPCTGVLKLSASGTVPCVRRLEGFNAKAFLFVPDSYWGSSDTVSVTVLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(25223. .25413,25596. .26220)
/gene="P0037C04.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVVAAFSSSSRRLPSSSPLSSPTPAAELAFSLAGRRARLLSRRPRRPSSSPPLSSPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\it LARCREGARRRGRQAAGQRHSGRQGSNESTTQSQPTVTVIEDLKLEIGKLANRRGRRA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAB55520.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MDNTGTPKRTRWSENKAQQDGKDETTKLTYSIERDALECPICFV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="hypothetical protein"
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                                 .35965,38859.
                                     . 39226))
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/product="putative Bowman Birk trypsin inhibitor"

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Search completed: October 5, 2002, 20:28:59 Job time: 9074 sec
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                                                                                                                                        Db 131915 GTGGAGGCGCCGCTCGGCCTCCCCTGCGGCGATGAGTTCGACCGCGTCCTCATGCTCGCC 131974
                                                                                                                                                                                                                                                                                                                                                                Db 131855 CTCACCCGCGCCAACCTCCTCGCCGGACTCCTCGGCGCCTACGTCATCCGCAACCCGGCG 131914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 131795 TAÇACCTACCCCAACGCGCAGTCCCCGGCGTGCTCTGGTACCACGACCACGCCCTCGGC 131854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.8%; Score 79.8; DB 8; Best Local Similarity 61.1%; Pred. No. 1.3e-08; Matches 129; Conservative 0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                      729 gaggatgccctgaacctccccagcggctacggcgagtttgatatccccttggttctgact 788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 609 tactaccccaacaggcaggctgcccgcatgctttggtaccatgaccatgccatgtcc 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(42298..43077)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(42298. .43077)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVESCAAACGOCEMVDSWSWRPLFVCRDSFTGDPGPRCTPEMHN"
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_Geneseq_032802:*
1: /SIDS1/gcgdata/gcg.
2: /SIDS1/gcgdata/gcg.
3: /SIDS1/gcgdata/gcg.
4: /SIDS1/gcgdata/gcg.
5: /SIDS1/gcgdata/gcg.
6: /SIDS1/gcgdata/gcg.
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Query
Match Length DB
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Gapop 10.0 , Gapext 1.0
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2095
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Copyright (c) 1993 - 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
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                                                                                     SUMMARIES
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Description
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immune.	AAK67293	S	31405	-	æ	5.
Human immune/haema		22	23457	1.9	œ •	.44
Polynucleotide		20	20757	1.9	8	43
N. meningitidis	AAA E	21	523	1.9	8	42
A. niger pH 2.5	AAQS	15	2071		9.	41
pH 2.5 acid phosph	AAQS	15	2071	1.9	39.4	40
Human immune/haema		22	15772		0.	39
Probe #8506 used		22	600		40.8	38
Human bone marrow		22	600		0	37
		22	600		0	36
Probe #6837 for ge		22	600	•	0	35
Human foetal liver		22	600		0	34
Human skeletal mus		22	2012		٢	33
Human immune/haema		22	68356		ω	32
Human immune/haema		22	68356	2.1		<u>ω</u>
Propionibacterium		23	61313	2.1	44	30
Gene encoding a		21	10732	2.1	44.8	29
Rat secreted expre		21	523		47.2	28
Rat secreted expre	AAA43363	21	523	2.3	47.2	27
C glutamicum codin		22	349980		49.6	26
Corynebacteriu		22	1614	2.4	50	25
C glutamicum codin		22	1533		in	24
Amerosporium atrum		21	858		~1	23
Amerosporium atrum		21	858	4.2	~1	22
Micromonospora		22	109519	4.6	(D	21
		21	2905	13.5	283	20
		21	2905	13.5	283	19
ba		21	2063		288	18
Curvularia palles		21	2063	13.7	288	17
tachybotrys		21	3677	4	9	16
		21	3677	٠.	300.4	15
		20	3677	14.3	300.4	14
tachybotrys	AAZ25	20	3676	14.3	300.4	13
	AAZ2760	20	2067	14.3	300.4	12
Stachybotrys chart	AAZ25735	20	2067	14.3	300.4	11
	AAZ2572	20	1791	21.9	458.8	10

ALIGNMENTS

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	intron		exon		intron		exon		intron		exon			CDS			Stachybotrys chartarum.		bleaching; ds.	detergent; paper	Stachybotrys phe		Stachybotrys cha		18-JUN-2001 (fi		AAF82586;		AAF82586 standard; DNA; 2095 BP.
/number= 3	16931745	/number= 3	9531692	/number= 2	870952	/number= 2	320869	/number= 1	268319	/number= 1		/product= "Stachybotrys phenol oxidase B"	/*tag= a	772016	Location/Qualifiers		rtarum.			<pre>detergent; paper production; pulp production; textile; food industry;</pre>	nol oxidase B; spoB; phenol oxidising enzyme;		Stachybotrys chartarum phenol oxidase B gene.		(first entry)				d; DNA; 2095 BP.

Stachybotrys chart	AAA51314	21	1791	22.0	460.4	9
Stachybotrys chart	AAA50019	21	1791	22.0	460.4	80
Stachybotrys pheno	AA227601	20	1791	22.0	460.4	7
DNA encoding 'a phe	AAZ61243	21	2110	24.7	517.4	6
Bilirubin oxidase	AAQ47790	14	1959	25.2	528.6	5
Stachybotrys chart	AAF82585	22	1958	92.8	1944.6	.~
Stachybotrys, chart	AAF30028	22	1958	92.9	1946.2	ω
Stachybotrys chart	AAF30029	22	2095	100.0	2095	2
Stachybotrys chart	AAF82586	22	2095	100.0	2095	1
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a Stachybotrys chartarum phenol oxidising enzyme. The invention relates to detergent compositions comprising one (more surfactants and a phenol oxidising enzyme having at least 68% identity to the Stachybotrys chartarum phenol oxidising enzyme. Phenol oxidising enzymes may be used in the detergent, paper, pulp, textile and food industries. They are used for preventing the transfer of dyes in solution from one textile to another during detergent washing, or in modifying the colour associated with dyes and coloured compounds having different chemical structures, such as in pulp and paper bleaching, bleaching the colour of stains on fabric and in detergent and textile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNIL )
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in detergent or cleaning finishing or production, processing applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000;
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The present sequence is that of the Stachybotrys chartarum MUCL 388 spoB gene encoding phenol oxidase B (see AAB20097). The gene was isolated by PCR using primers (see AAB2003-31) based on 2 peptide fragments of the isolated enzyme. The invention provides phenol oxidising enzymes such as phenol oxidase B, or enzymes with at least 68% identity to it, nucleic acids encoding them, expression vectors, filamentous fungus and yeast host cells, and methods for the recombinant production of the phenol oxidising enzymes. The enzymes are useful for bleaching of pulp and paper, fabric stains, and in detergent and textile applications. They show optimal activity at pH 5-11, 7-10.5 or 8-10, and 20-60 or 20-40 degree C.
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The present sequence encodes a Stachybotrys chartarum phenol oxidising enzyme. The invention relates to detergent compositions comprising one more surfactants and a phenol oxidising enzyme having at least 68% identity to the Stachybotrys chartarum phenol oxidising enzyme. Phenol oxidising enzymes may be used in the detergent, paper, pulp, textile are
                                                                  in detergent or cleaning finishing or production, processing applications
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P-PSDB; AAR40843.
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The present sequence encodes a phenol oxidizing enzyme from t fungus Acremonium murorum. The enzyme has the CBS accession n 157,72. The enzyme catalyses redox reactions and is specific molecular oxygen as the electron acceptor. The phenol oxidisi
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RESULT
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XX 16-DEC-1999 AAZ27601; AAZ27601 standard; (first

1791

ВP

Stachybotrys phenol oxidase

entry)

coding sequence

Phenol oxidase;
fabric washing; enzyme; coloured compound; dye transfer prevention
stain bleaching; anti-dye transfer; detergent; ss.

Stachybotrys

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Matches 996
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22-DEC-1998;
22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....s sequence encodes the Stachybotrys chartarum phenol oxidase enzyme of the invention. The invention is used to modify a coloured compound a prevent dye transfer during fabric washing, or for stain bleaching or anti-dye transfer. It is useful in the detergent, paper and pulp, textiand food industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel enzyme for modifying dye-transfer -
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                                                                                                                                                 the S. chartarum phenol oxidising enzyme gene (see AAA50018), provide the enzymes are capable of modifying the colour associated with dyes or coloured compounds, and are produced from a bacterium, yeast or fungus (see AAY9538-40). The phenol oxidising enzymes can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. They may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidising enzyme, methods for producing the phenol oxidising enzyme, and methods for constructing expression hosts are provided.
                                                                                                                                                                                                                                                                      The present sequence is that of the Stachybotrys chartarum MUCL 038898 cDNA encoding a phenol oxidising enzyme (see AX95537). The invention relates to detergent compositions comprising novel phenol oxidising enzymes that are encoded by nucleic acids capable of hybridising to
                                                                                                                                                                                                                                                                                                                                               Detergent composition comprising novel phenol oxidising enzyme from fungus or bacteria, useful for pulp and paper bleaching, l color of stains on fabric and for anti-dye redeposition -
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1791 BP;
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Best Local Similarity
Matches 957; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detergent
to bleach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a detergent composition containing a purified phenol oxidising enzyme derived from Stachybotrys. The present sequence represents a PCR fragment of Stachybotrys chartarum phenol oxidising enzyme. The enzyme can be used to modify the colour of dyes and other coloured compounds (e.g. for use in pulp and paper bleaching also for removing stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye transfer during fabric washing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Convents D, Wang C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-1998;
22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2067 BP; 445 A; 621 C; 500 G; 501 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 17; Fig 9;
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Pred. No. 2.4e-74;
0; Mismatches 501
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                       This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme of the invention. The invention is used to modify a coloured compound prevent dye transfer during fabric washing, or for stain bleaching or anti-dye transfer. It is useful in the detergent, paper and pulp, text
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RESULT 1
AAZ25728
ID AAZ2
XX AAZ2
XX O5-J
XX Stac
XX S Stachybotrys chartarum; phenol oxidising enzyme; colour; detergent; anti-dye transfer; stain removal; bleaching; Stachybotrys AAZ25728 standard; DNA; 3676 05-JAN-2000 (first entry) chartarum phenol oxidising enzyme ВP

genomic

24-MAR-1998; 22-DEC-1998; 23-MAR-1999; Stachybotrys 30-SEP-1999 98US-0046969 98US-0218702 99WO-EP02042

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Best Local Similarity
Matches 957; Conser
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22-DEC-1998;
22-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21;
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The present sequence is that of the Stachybotrys chartarum MUCL 38898 cphenol oxidising enzyme gene, including promoter and terminator sequences. The gene was isolated from genomic DNA using primers (see AAA50023-24) based on isolated peptides of the enzyme. The relates to detergent compositions comprising novel phenol oxidising correlates to detergent compositions comprising novel phenol oxidising to the present DNA sequence, provided the enzymes are capable of hybridising to modifying the colour associated with dyes or coloured compounds, and are produced from a bacterium, yeast or fungus (see AN95539-40). The phenol oxidising enzymes can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. They may also be capable of modifying the colour in the absence or presence of an cenhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidising enzyme, methods for producing the phenol oxidising enzyme, and methods for constructing expression to hosts are provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition -
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ALIGNMENTS

ORIGIN	BASE COUNT	*								source	FEATURES									COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	RESULT 1 BE188240	
	131 a 176 c 162 g 128 t 3 others	supplemented with hydrogen peroxide"	cultures grown in liquid B5 for 48 hours and transferred	/note="Vector: Lambda bluescript; A mixture of mycelial	<pre>/tissue_type="Mycelium"</pre>	/clone_lib="In vitro expressed cDNAs"	/db_xref="taxon:5499"	/strain="Race 4"	/organism="Cladosporium fulvum"	1600	Location/Qualifiers	POLYA=No.	High quality sequence stop: 600	Email: roliver@central.murdoch.edu.au	Fax: +61-8-9360-6303	Tel: +61-8-9360-7404	SABC, Perth 6150, Western Australia	Murdoch University	Necrotrophic Phytophatology Research Centre	Contact: R.P.Oliver	Unpublished (2000)	In vitro expressed genes of Cladosporium fulvum	Clark, A.J., Rasmussen, S.W. and Oliver, R.P.			Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et	Cladosporium fulvum	Cladosporium fulvum.	EST.	BE188240.1 GI:8667479	BE188240	oxidase precursor, mRNA sequence.	n vitro expressed cDNAs Cladosporium fulvum	BE188240 600 bp mRNA linear EST 25-SEP-2000		

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Murdoch University
SABC, Perth 6150, Western Australia
Tel: +61-8-9360-7404
Fax: +61-8-9360-6303
                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes Chaetothyriomycetes incertae sedis; Mycosphaerellaceae; mitosphycosphaerellaceae; Cladosporium.
                                                                                                                                                                                                                                                      In vitro expressed genes Unpublished (2000)
                                                                                                                                                                                                                                                                  Clark,A.J., Rasmussen,S.W. and Oliver,R.P.
In vitro expressed genes of Cladosporium fulvum
                                                                                                                                                                                                                                                                                                                                                    Cladosporium fulvum
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                                                                                                                                                                                                                                                                                                                                                                                              BE187716
BE187716.1 GI:8666955
                                                                                                                                                                                                                                                                                                                                                                                                                        BILOX In vitro expressed
Bilirubin oxidase precurs
                                                                                                                               POLYA-No
                                                                                                                                           High quality sequence
                                                                                                                                                         Email: roliver@central.murdoch.edu.au
                                                                                                                                                                                                                                          Contact: R.P.Oliver
                                                                                                                                                                                                                                                                                                                                                                      Cladosporium fulvum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE187716
                                                                                                                                                                                                                                                                                               (bases 1 to 700)
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/strain="Race 4"
/db_xref="taxon:5499"
/clone_tb="In vitro expressed cDNAs"
/clone_type="Mycellum"
/note="Vector: Lambda bluescript; A m:
cultures grown in liquid B5 for 48 hou
                                                                                  /organism="Cladosporium fulvum'
                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                          precursor, mRNA
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Pred. No. 4.8e-11;
0; Mismatches 178;
                                                                                                                                           stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                       700 bp mRNA linear EST CDNAs Cladosporium fulvum cDNA
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8 hours and to
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REFERENCE
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BE188099
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Best Local S
Matches 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gttgaggcccactacgctcctt 1688
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                                                                                                                                                                                                                                                                                                             EST.
Cladosporium fulvum.
Cladosporium fulvum
                                                                                                                                                                                                    1 (bases 1 to 664)
Clark,A.J., Rasmussen,S.W.
In vitro expressed genes of
Unpublished (2000)
                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes
Chaetothyriomycetes incertae sedis; Mycosphaerellaceae; mitos
Mycosphaerellaceae; Cladosporium.
                                                                                                                                                                                                                                                                                                                                                                                                        BE188099 664 bp mRNA line
CFC377-R In vitro expressed cDNAs Cladosporium
                                                                          High
                                                                                                                         SABC, Perth 6150, Western Tel: +61-8-9360-7404
                                                                                                                                                      Murdoch University
                                                                                                                                                                                       Contact: R.P.Oliver
                                                                                                                                                                                                                                                                                                                                                               BE188099.1
                                                                                                                                                                                                                                                                                                                                                                            to Bilirubin oxidase
BE188099
                                                                                            Email: roliver@central.murdoch.edu
                                                                                                          Fax: +61-8-9360-6303
                                                                                                                                                                      Necrotrophic Phytophatology
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/organism="Cladosporium
/strain="Race 4"
                              1. .664
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183 g 146 t 7 others
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No. 5.3e-11;
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TITLE
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Matches
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EST0376 Triticum aestivum Lambda
JA1_5A_A06_T3 5', mRNA sequence.
                                                                                                                                                                                                                             1150 Lilly Hall, Tel: 765-494-5565
                                                                                                                                                                                                                                                                         Contact: Anderson, J.M.
Crop Production & Pest Control Research Unit
                                                                                                                                                                                                                                                                                                         homolog in wheat
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                       Anderson, J.M., Williams, C.E. and Goodwin, S.B. Analysis of an EST database reveals a probable
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE216983.1 GI:8904523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JA1_5A_A06_T3
BE216983
                                                                                                                                                                                                                Fax: 765-496-2926
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                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 848)
                                                                                                                                                                              primer: T3
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     139
                                                                                                                                                             quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                           janderson@purdue.edu
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174 c 174 g 140 t 27 others
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/clone_lib="In vitro expressed cDNAs"
/tissue_type="Mycelium"
                                              /clone="JA1_5A_A06_T3"
/clone_lib="Triticum aestivum Lambda
                                                                                                   /strain="P29"
                                                                                                                /organism-"Triticum aestivum"
   /dev_stage="9 day old seedlings"
312 c 263 g 134 t
                                 /tissue_type="leaf"
                                                                              db_xref="taxon:4565"
                                                                                                                                            ocation/Qualifiers
                                                                                                                                  .848
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                                                                                                                                                                                                                                                                                                  Email: rwing@clemson.edu

Email: rwing@clemson.edu

Total hq bases = 260

Total hq bases = 260

Seq primer: AATTAACCCTCACTAAAGGG

Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF264805 880 bp mRNA
HV_CEa0010G19f Hordeum vulgare seedling
HVcDNA0004 (Blumeria challenged) Hordeum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
On Nov 17, 2000 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV_CEa0010G19f, mRNA sequence.
BF264805
BF264805.2 GI:13261741
                                                                                                                                                                                                                                                                                                                                                                              Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for barley genomics: Blumeria infected incompatible (Mla13) seedling leaf cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                     100 Jordan Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticeae; Hordeum. (bases 1 to 880)
                                                                                                                                                                                                                                                                                  quality sequence stop:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       University Genomics Institute
             C.I. 16155 (Mial3) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate A27 (AvrMla13) of Blumeria graminis f. sp. hordei, and leaves were
                                                                                                                         /db_xref="raxun:"-----/clone="HV_CBa0010G19f"
/clone="HV_CBa0010G19f"
/clone_lib="Hordeum vulgare seedling green
library HVcDNA0004 (Blumeria challenged)"
                                                                                          /tissue_type="seedling green leaf"
/lab_host="TJC121"
/note="Yector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                                                                                                                                                                                                          /organism="Hordeum vulgare"
/cultivar="CI16155 (Mla13)"
/db_xref="taxon:4513"
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Pred. No. 1.1e-05;
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and snap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCGACCGCGACTTCATGCGCGACGGCGCGCTCTTC
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                                                                                                                                                                                                                                                                                                              Sorghum propinquum.
Sorghum propinquum
Sorghum propinquum
Sorghum propinquum
Sorghum propinquum
La Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG053739 465 bp mRNA linear EST 25-JAN-200:
|RHIZ2_9_B08.b1_A003 Rhizome2 (RHIZ2) Sorghum propinguum cDNA, mRNA
                                                   Tel: 706 542 1860 Fax: 706 542 1805
                                                                                               The University of Georgia Plant Sciences Building, I
                                                                                                                                                   Contact: Cordonnier-Pratt Department of Botany
                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                          Cordonnier-Pratt,M.-M., Gingle,A., Paterson,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG053739.1 GI:12509741
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21; Conservative
                                                                                                                                                                                                                           EST database from Sorghum:
il: mmpratt@uga.edu
primer: JEN REV
                                                                                                                                                                                                                                                                                                      (bases 1 to 465)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html%"
198 c 318 g 149 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library was made, and 1 million pfu were in vivo
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Pred. No. 4.1e-05;
0; Mismatches 96;
                                                                                                    Rn.
                                                                                                  2502,
                                                                                                                                                                                                                        Sorghum propinguum rhizomes
                                                                                                  Athens, GA 30602-7271, USA
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TITLE
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BASE COUNT ORIGIN

Matches Query Match

RESULT 6
BG053739/c

DEFINITION

KEYWORDS VERSION

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gccaagcgatacaacgcagacggcactctcttc 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCACCCGCGCCAACCTCCTCGCCGGCCTCCTCGGCGCCCTACGTCATCGAGAAGCCGGAG
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                                                                                                                                                                                                                                                                                       The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamuekazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. Generation of 7137 non-redundant expressed sequence tags legume, Lotus japonicus DAR Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yasukazu Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lotus japonicus
Lotus japonicus
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      81
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/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
a 100 c 68 g 62 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 128 c 193 g 72 t
                                                                                                                                                                              /organism="Lotus japonicus"
/db_xref="taxon:34305"
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/db_xref="taxon:132711"
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56.8%;
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its (two-week old)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAGACCTATCACTACCCAAACAACCAACCAGGAAATCTATGGTACCATGACCATG
                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified lPs phage vector (Mo bi Tec, Germany). 5' end of the CDNA that was digested with Xhol was: ligated to SalI site of the vector and the 3' end including pblyA tail was ligated to BamHI site of the vector. cDNA instert could k amplified with conventional T7 and T3 primers. This full-length cDNA ilbrary was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light.
                                                                                                                                                                                                                                                                                                                                                                                             Tel:
Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BJ159802 580 bp
BJ159802 full length cDNA library,
gametophores Physcomitrella patens
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Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Eukaryota, Viridiplantae; Streptophyta; Embryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physc
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BJ159802
BJ159802.1 GI:18327798
EST.
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, Carninci,P., Hayashizaki,Y., Shinozaki,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                               National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center For Genetic Resource Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
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                124
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81-559-81-6856
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              gametophores with 2 to 5 138 c 170 g 148
                                                                 young gametophores"
                                                                                /clone_lib="full length cDNA library,
                                                                                                   /clone="pph17c15"
                                                                                                                  /organism="Physcomitrella patens subsp. patens'/db_xref="taxon:145481"
                                                                                                                                                                          Location/Qualifiers
                                                  /tissue_type="mixture of chloronemata
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0; Mismatches
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Pred. No. 0.023;
0; Mismatches 106;
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s subsp. patens
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K., Kohara,Y.
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Physcomitrella.
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Query Match

2.48;

Score

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DВ

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Length 580;

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Best Local Similarity
Matches 156; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST I
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y., Person, B., Swaller, T., Gibbons, M., Papé, I., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., R., Waterston, R. and Wilson, R.
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shoemaker, R., Keim, P., V., A., Bolla, B., Marra, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max
                                                                                                                                                                                                                                                                                                                                                                                        www.resgen.com
Seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wylie
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                                                                                                                                                                         /organism="Glycine max"
/db_xref="taxon:3847"
/tissue_type="seedlings
(Sudden Death Syndrome)
                                                                                       /clone="SOYBEAN CLONE ID: Gm-c1072-2563"
/clone_lib="Gm-c1072"
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/dev_stage="2-3 weeks old" /lab_host="DH10B"

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                      BG526127
BG526127.1
EST.
Contact: Jim Brandle
Genomics and Biotechnology
Agriculture and Agri-Food (
                                                                                                                  1 (bases 1 to 766)
Brandle, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.
Leaf ESTs from Stevia rebaudiana: A resource for gene of
                                                                                                                                                                                                                                     Stevia rebaudiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG526127 766 bp mRNA linear F 56-88 Stevia field grown leaf cDNA Stevia rebaudiana
                                                                                 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                          Stevia rebaudiana.
                                                                                                                                                                                                                          Heliantheae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SK(+)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of SDS (Sudden Death Syndrome) disease by the translocation of culture filtrate of Fusarium solani {\bf f}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp. glycines (Plant Cell Report 18:375-380). Cultivar PI. 567374 is partially resistant to the disease SDS. Plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                       781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 acaaggattactacccccaacaggcaggctgcccgcatgctttggtaccatgaccatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acceggetgaggatgecetgaacctececageggetaeggegagtttgatateeeettgg
                                                                                                                                                                                                                                                                                                                                                                                                 TCGTATTTG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccatgtccatcaccgccgagaacgcctacatgggtcaggctggtgtctacatgatccagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAANGNCCTACGACTACCACCAACCAACAACAGCCCGGCAACCTTTATTACCATGATCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                     ttctgactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCACGATGTCGAAGCCCCACTTGGGCTCCCTTCTGGTGATGAGTTTGATCGGCCGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100;
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                Mammalia; Eutheria;
1 (bases 1 to 286)
                                                                                                                                            Mus musculus
                                                                                                                                                                                         SSD
                                                                                                                                                                                                                             DNA sequence.
A2714471
                                                                                                                                                                                                                                                                     AZ714471
RPCI-24-138E2.TJ RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: brandleje@em.agr.ca
Seq primer: T3 promoter pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1391 Sandford St.
Tel: 519 457 1470
Fax: 519 457 3997
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                            AZ714471.1
                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The cDNA was prepared using an Xho1-poly(dT) linker-primer. An EcoRI adapter was ligated to the blunt end cDNA and the products were digested with EcoRI and XhoI enabling directional cloning into the lambda ZAP Express vector. The library was amplified using the host strain XLI-Blue MRF'. Mass excision of the library was performed to obtain pBK-CMV phagemid clones in the host strain XLOUR. Single pass DNA sequencing was performed using the T3 promoter primer: 5' ATTAACCGCACTAAAGGGA 3'. This library was constructed by Alex Richman."
                                                                                                                                                                                                                                                                                                                                                                                                                                       789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xret="taxu::Ju,"
/db_xret="taxu::Ju,"
/clone_lib="Stevia field grown leaf cDNA"
/tissue_type="leaf"
/dev_stage="field grown, mid-size"
/lab_host="E. coli strain xLoLR"
/lab_host="E. coli strain xLoLR"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from polyA+ enriched mRNA from field grown leaves. Mid-size actively growing leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Stevia rebaudiana"
/strain="751/1501"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Landrace"
                                                                                                                                                                                                          GI:12450418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3%;
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                                                                                                        Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47.8; DB Pred. No. 0.33;
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Mus musculus
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                                                                                                        Sciurognathi; Muridae; Murinae;
                                                             Shatsman, S., Akinret, B., Levins, M.
                                                                                                                                                                                                                                                                                             DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                          GSS 24-JAN-2001
RPCI-24-138E2,
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                                                             REFERENCE
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                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                          AUTHORS
                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                              216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543 tctttctctcgagctccctttgatggttgggctgaggacactacccagcctggcgagtac 602
                                                                                                                                                                                                                                                                                                                                                                                                                              723 ccggctgaggatgcc 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaggattactactaccccaacaggcaggctgcccgcatgctttggtaccatgaccatgco 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atgtccatcaccgccgagaacgcctacatgggtcaggctggtgtctacatgatccaggac 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTACCCTCACCATCTACAACGCCAACATCGACGATGCCGGCATATACAAGTGTGTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGAGAAGCTGAGCCCAAACCAGCAGCGGATCTCAGTGGTGTGGAATGATGACTTCTTC 155
                Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea;
Triliceae; Hordeum.

1 (bases 1 to 599)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
                                                                                                                                                                                                                                           D99 bp mRNA linear EST 22-DCT-2001 HVSMEf0015p2lf Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                     BF258534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 138 row: E column: 2
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                                                                                                                                                                              EST
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Class: BAC ends
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Contact: Shaying Zhao
                                                                                                                                                            barley.
                                                                                                                                                                                                 BF258534.2
                                                                                                                                                                                                                                   HVSMEf0015P21f, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhao@tigr.org
                                                                                                                                        Hordeum vulgare
Henry,D., Palmer,M., Rambo,T.,
., Oates,R. and Main,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/60"
/db_xref="taxon:1090"
/clone="RPCI-24-138E2"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Cell_type="Spleen/Brain" /Cell_type="Spleen/Brain" /Cell_type="Spleen/Brain" /Note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; /Note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; /Note="Vector at the pTARBAC1 cloning vector at the library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.2%;
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953 aacggtcagccttggcctatgctcaacgtgcagccgcaagtaccgcttccgcttcctc 1012
                                                                                                                                                                                       aacgctgccgtctcacgctctttcgctctgtatcttgctacct--ctgaggattcagaga 1070
GTCGGCTCCGACTCCGTGTACCTCGCCCGGCCGGTGCCCACGGAGGGGTTCCTGCTCGCG
                                                   ccagacttcccttccaggtcattgccgctgacggtggtctgcttgagggccctgttgaca 1130
                                                                                                                                                                                                                                                            AACGGCAAGGCCTGGCCGTTCCTCCGCGTGCGGCGCCGCCGCCTACCGCTTCCGCATCCTC 136
                                                                                                                                Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library Unpublished (2001)
On Nov 16, 2000 this sequence version replaced gi:11187647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 Jordan Hall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total hq bases = 451
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: AATTAACCCTCACTAAAGGG h quality sequence stop: 552.
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gpages/bgn/31/cover.html)"
a 215 c 206 g 82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give palluescript SK(-) cDNA phagemids. These steps were performed in the TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oat Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
Seeds were surface sterilized then germinated under axenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this clone see http://www.genome.clemson.edu/orders Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Seedling root"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Hordeum vulgare seedling root EST library
HVcDNA0007 (Etiolated and unstressed)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genome.clemson.edu/projects/barley. To order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="HVSMEf0015P21f"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of almonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alžawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koud,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., M., Kozaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagamu,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB655683 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130015D23 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Konno, H., Fukunishi, Y.,
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                                                                                              prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
Genomic Sciences center and serious transl Research in Riken RIKEN. Division of Experimental Animal Research in Riken was
                                                                                                                                                                                                                                                                                                                                                                                                                                       spinal ganglion"
                                                                                                                                                                                                                                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                            /dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RIKEN full-length enriched, 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus_musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="D130015D23"
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uJ35b06.yl Sugano mouse kidney mkia Mus musculus
IMAGE:1921907 5′ similar to gb:Y00051 Mouse mRNA
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Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                             Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Other_ESTs: uj35b06.x1
                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI876848
                                                                                                                                                                                                         This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI876848.1
                                                                                                                                                                                        IMAGE Consortium (info@image.linl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 485)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." a 180 c 179 g 142 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                      /organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1921907"
/clone_lib="Sugano mouse
                                                                                                                        Location/Qualifiers
                                                                                                                                                  custom
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                                                                                                                                               primer used
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                                                                                                                                                                                                                                                                                             Louis, MO 63108, USA
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for neural cell
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kidney mkia"

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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Best Local
                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 102;
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                                                                                                                                                                                                                                                                                               1 (bases 1 to 562)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A, Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagama,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus
BB651243
                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB651243 RIKEN full-length enriched, 0 day neonat musculus cDNA clone C230070H21 5', mRNA sequence
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.,
                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB651243.1 GI:16485497
                                                                                         Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a Draili adaptor [TGTTGCCTACTGG], digested and cloned into distinct Draili sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for; sequencing: 5' end primer CTTCTGCTCTAAAAGCTTGCG and 3' end primer CGACCTGCAGCACA."
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: kidney; Vector: pME18S-FL3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.2%;
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Pred. No. 0.9;
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SOURCE VERSION

KEYWORDS

COMMENT

Sugahara,Y.,

Shibata, K.,

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  423
                                                                                                                                                                                                          303 CTTCCTGTGTCAAGTGGCAGGAGATGCCAAAGATAAGGACATCTCCTGGTTCTCCCCCAA 362
                                                                                                                                                                                                                                                                                                                    Local Similarity 52.
                                catgtccatcaccgccgagaacgcctacatgggtcaggctggtgtctacatgatccagga 721
                                                                                                      TGGGGAGAAGCTGAGCCCAAACCAGCAGCGGATCTCAGTGGTGTGGAATGATGACGACTC 422
caaggattactactaccccaacaggcaggctgcccgcatgctttggtaccatgaccatgc 661
                                                                                                                                                                                                                                                           ctctttctctcgagctccctttgatggttgggctgaggacactacccagcctggcgagta 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Sequence. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Genome Sequences. Mamm. Genome. 12,
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Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with tuman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="0 day neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="C230070H21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="cerebellum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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Db 483 CACGGCTGAGGACGGC 498

Search completed: October 5, 2002, 18:54:25 Job time: 3515 sec

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Result
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 seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic search, using sw model
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

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ALIGNMENTS

CURRENT APPLICATION NUMBER: US/09/401,476 CURRENT EILING DATE: 1999-09-22 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 LENGTH: 2095 TYPE: DNA ORGANISM: Stachybotrys chararum US-09-401-476-3 APPLICANT: Wang, Huaming TITLE OF INVENTION: No. FILE REFERENCE: GC584 US/09401476 6168936el Phenol Oxidizing

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Mismatches 0,

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Sequence 1, Application US/09401476
Patent No. 6168936
GENERAL INFORMATION:
APPLICANT: Wang, Huaming
TITLE OF INVENTION: No. 6168936el Phenol Ox
FILE REFERENCE: GC584
CURRENT APPLICATION NUMBER: US/09/401,476
CURRENT FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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RESULT 3
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHRIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.2
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RESULT 4
US-07-923-724-1
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                                                                                                       GENERAL
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
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     APPLICANT:
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LENGTH: 7218 base pair
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REGISTRATION NUMBER: 29,768
REGERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
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                                                          Paloheimo, Marja T.
Miettinen-Oinonen, Arja S.K.
                                           Torkkeli, Tuula K.
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 07
FILING DATE: 19-MAR-1990
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SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
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APPLICANT: Fagerstr m, Richard B.
TITLE OF INVENTION: Production of Phytase
TITLE OF INVENTION: in Trichoderma
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 29-APR-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                 515
                                                                                                                                                                                                                                                                                                     455 catcatcgttcctcgtggcactgagagtgttgtccgcttcgtgaacagcggagagaacac 514
684 CGGTGAGGGTTTCTTTGGCTACAACTACTCCACCAACGCTGCCCTCAACATCATCTCCGA
                   695 tcaggctggtgtctacatgatccaggacccggctgaggatgccctgaacctccccagcgg 754
                                                                                                                                                                                                            504 CGTCCCTAATGAGTGCTACTACAACGCCGAGACCACCAGCGGCCCCTACGCCGGTTTGCT 563
                                                                                                                                                                                                                                                                               444 CAGCATCAACACTACTGAATACAAGGGCGACCTGGCCTTCCTGAACGACTGGACCTACTA 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                    GACGGTCGTGCCCTTCTTTTCTAGTGGCTACGGACGTCATCGAGACGGCCCGCAAGTT
                                                                                            ccgcatgctttggtaccatgaccatgccatgtccatcaccgccgagaaacgcctacatggg 694
                                                                                                                                                           139;
                                                                                                                                         GGACGCGTACAACCATGGCAACGATTACAAGGCTCGCTACGGCCACCTCTGGAACGGTGA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H: 2071 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cimbala, Michele A
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                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(136..915, 970..1089, 1142..1245, 1305..1737)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sterne,
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                                                                                                                                                                                                                                                                                                                                                   Score 39.4; DB 1;
Pred. No. 0.088;
0; Mismatches 166;
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US-08-609-426A-1
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US-08-609-426A-1
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Query Match 1.9
Best Local Similarity 45.6
Matches 139; Conservative
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                                                                                                                                                                                                 TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
                                                                                                                  FEATURE:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                 join(136..915, 970..1089, 1142..1245, 1305..1737)
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29-APR-1987
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                1.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version
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Score 39.4; DB 2;
Pred. No. 0.088;
0; Mismatches 166;
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                          Length 2071;
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 Gaps
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RESULT 6
US-08-374-652C-3
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                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-UL-1992
                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,652C
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT:
                                 ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 27-JUL-1993
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ELECOMMUNICATION INFORMATION:
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         REGISTRATION NUMBER: 41.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 20005
                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                              WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOUSTON, CHRISTINE
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                                                                                                                                                                                                                                                                                                                Floppy disk
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ENZYMES
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                       41,264
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MARJA T.
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           050.071001
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INFORMATION FOR SEQ ID NO:

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TELEPHONE:

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US-09-007-005-17/c

: Sequence 17, Application US/09007005B

: Patent No. 6258558
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US-08-374-652C-3
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Best Local Similarity
Matches 139; Conserv
                                                                                                                                                                                  SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SELECTION OF PROTEINS (
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
                                                                                                                   LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
                                                                               FEATURE:
OTHER INFORMATION: Translation
                FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(289)
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TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
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ION: (1)...(289)
INFORMATION: n
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                                                                                                                                                                                                                                                                                                                                                                                                           SELECTION OF PROTEINS USING RNA-PROTEIN
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  A,T,C
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; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C
US-09-244-796-17
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: Sequence 17, Application US/09244796

: Patent No. 6281344
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SEQ ID NO 17
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                       1.8%;
Best Local Similarity 4.9%;
Matches 10; Conservative of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SELECTION TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350007
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ORGANISM: Artificial Sequence
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                                                           1660 tgtctatgttgaggcccactacgctcctttcccgtaagttctcgccttttacctaactgg 1719
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les 10; Conservative
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                                                                                                                                            tgtctatgttgaggcccactacgctcctttcccgtaagttctcgccttttacctaactgg
YSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYCYAYTYTYGYTYAYAYT 40
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93; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37.6; DB 4;
Pred. No. 0.09;
93; Mismatches 101;
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                                                                                                                                                                          Matches
                                                                                                                                                                                         Best Local
                                                                                                                                                                                                       Query Match
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APPLICATION NUMBER: US 08/
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: US 08/
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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APPLICANT:
1944 cactgaccgcattcaggagatggctagcttcaacccctacgcccaggctgatgatg 1999
                                                                          1884 ccgccccttcctcctcggagagttcgagaatggctcgggtgacttcagcgagcttgccat 1943
                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: JP 156399/1994 FILING DATE: 16-JUN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                               198
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                                                   258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                EENGTH:
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                                             CACGCCTTCCTCGACGGCGCGCACGAGCGCGGGGATCCGGGTGATCATCGACTTCCTCAT 317
                                                                                                          CGGGTACGACGTCGCCGACTACACCGGGGATCCTCCCGGAGATCGGCACGGTCGAGGACTT 257
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5. 5763228
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SUGIMOTO, TOShiyuki
SURITON: RECOMBINANT ENZYME FOR CONVERTING
VENTION: MALTOSE INTO TREHALOSE
                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                 linear
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50.0%;
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P-1995
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Pred. No. 1.5;
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US-08-528-199-5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 08/485,126
APPLICATION NUMBER: US 08/485,126
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: US 08/485,126
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                 1884 ccgccccttcctccggagagttcgagaatggctcgggtgacttcagcgagcttgccat 1943
                                                                                                                                REFERENCE/DOCKET NUMBER: KU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHAX: 202-737-3528
1944 cactgaccgcattcaggagatggctagcttcaaccccctacgcccaggctgatgatg 1999
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                                                                                                                                                                                                                                                                                                      FEATURE:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                               CCACGCCTTCCTCGACGGCGCGCACGAGCGCGGGGATCCGGGTGATCATCGACTTCGTCAT 317
                                                                                                          CGGGTACGACGTCGCCGACTACACCGGGGATCCTCCCGGAGATCGGCACGGTCGAGGACTT 257
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/ENTION: RECOMBINANT ENZYME FOR
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318 GAACCACACGAGTGACGCGCACCCGTGGTTCCAGGCCTCCCGCAGCGATCCCGACG

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Best Local Similarity
                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: SKINBI
CLONE: 1869688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                         813 GCCCTGGCTGAGCATGATGTTCTCGGGCTTGAGGTCCCGGTAGATGATGCCCTGGGA 754
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                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                ctccccagcggctacggcgagtttgatatccccttggttctgactgccaagcgatacaac 803
                                                                                                                                             gcctacatgggtcaggctggtgtctacatgatccaggacccggctgaggatgccctgaac 743
GAAGATGCCCTCTCGCTCCAGATGCGTGAAGAGCTCGCCACC 652
                          gcagacggcactctcttctccaccaatggagaggtttccagc 845
                                                                                                                                                                                      {\tt AGTGACGCCCCTCATGGATAGACTCCTTGCAGAGTCCAAAGTCGGTCAGTTTGATGTG\cdot 814}
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47.38;
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                                                                                                                                                                                                                                                     Score 34.8; DB 2;
Pred. No. 1.9;
D; Mismatches 117;
                                                                                                                                                                                                                                                                                  Length 1637;
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Best Local Similarity
"~+~hes 90; Conserv?
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ZIP: 2005-3910

ZIP: 2005-3910

COMPUTER READABLE FORM:

COMPUTER: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

PC-DOS/MS-DOS

PC-DOS/MS-DOS

PC-DOS/MS-DOS
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                                                                    1230
                                                                                                                                      1290 CCCGATCGCCAGCGACAACTTCTACTACCCCGGCTACGCTGGCATTGGCACCCAACTCCA 1349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 8
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 09-MAY-1990
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OPERATING SYSTEM: PC-DA
SOFTWARE: PATENTIN Rela
CURRENT APPLICATION DATA:
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                            776 cttggttctgactgccaagcgatacaacgcagacggcactctcttctccaccaatggaga 835
                                                                                                    716
                                                                                                                                                                     656 ccatgccatgtccatcaccgccgagaacgcctacatgggtcaggctggtgtctacatgat 715
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                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
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                                                                                    ccaggacccggctgaggatgccctgaacctccccagcggctacggcgagttttgatatccc 775
                                                                    CCTGACCCAGCCCGTGAACGGCGTGCCCCGCGTGGACTTTCACTGGAAGTTCGTGACCCA 1289
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09-MAY-1989
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Pred. No. 2.3;
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Best Local Similarity 43.6%;
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Patent No. 5716805
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                                                       1418 gctaatggacagtggacaatcaacggagttaccttctcggatgtcgagaaccgtctgctc 1477
                                                                                                                 1358 gagggcggcaactgggaccccgcaaaccccactgatgacgagactttcaccttcggccgt 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
1478 cgcaatgtgccccgcgacactgttgagatctggcgacttgagaacaactccaacggttgg 1537
                                                                                                                                                                                                                                                                                                FEATURE:
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ORGANISM: Mou
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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APPLICANT: Srinivasan, Subhashini
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                                 714 GACAAACACAGAAGCACCAGCTTGTAATTCAAACACTCCGCCCAAGTGAACAGACTGCTG 655
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                                                                                                                                                                                                                                                                                                               STRAIN:
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FILING DATE: 08-13-93
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                                                                                                                                                                                                                                                                                  NAME/KEY:
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TOPOLOGY: lir
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                                                                                               153; Conservative
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                                                                                                                                                                                Score 34.2;
Pred. No. 1
                                                                                                                                                               Mismatches 198; Indels
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                                                                                                                                    TELEFAX: 2065870606 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Apple Operating System SOFTWARE: Microsoft Word for Apple, versicurrent APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
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              HYPOTHETICAL:
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CORRESPONDENCE ADDRESS:
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ANTI-SENSE:
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                                                             STRANDEDNESS:
                                                                                                                                                                                                                      NAME: Perkins, Patricia REGISTRATION NUMBER: 34
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                                                   POPOLOGY:
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                                                                                                   ENGTH:
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US-08-249-189-1
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Best Local Similarity 43.6%;
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                                                                                                                                                                                                                               OFERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple OPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1658 gttgtctatgttgaggcccactacgctcctttcccgtaagttctcgccttt 1708
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                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01
FILING DATE: June 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: MOUSE IMMEDIATE SOURCE: CLONE: CD40-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 51 UNI
CLASSIFICATION:
                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ce 1, Application US/08484624A
No. 5962406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgcaatgtgccccgcgacactgttgagatctggcgacttgagaacaactccaacggttgg 1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAGCAGAAGGTGACTTGAGTGTAGACATAATAGAGTCCTTCTCTTTTAACCGGTCAGCTG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGCTGGGCTTCAGCCAGAGGCCGACGATGAATGGGCGTTGACTCGAAGGCTCCCGAT# 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      actcaccctgttcacattcacctcgttgacttccgagtcctttctcgttccactgcccgt 1597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACAAACACAGAAGCACCAGCTTGTAATTCAAACACTCCGCCCAAGTGAACAGACTGCTG 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gctaatggacagtggacaatcaacggagttaccttctcggatgtcgagaaccgtctgctc 1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 UNIVERSITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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GIBSON, MARYLOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FANSLOW, WILLIAM
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                                                                    08/477,733
                                                                                                                                                                                                                US/08/484,624A
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Pred. No. 1.8;
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Best Local Similarity 43.6
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      1418 gctaatggacagtggacaatcaacggagttaccttctcggatgtcgagaaccgtctgctc 1477
                                                                                                                                                                                                                                                                                                                                                      1358 gagggcggcaactgggaccccgcaaacccccactgatgacgagactttcaccttcggccgt 1417
                                                                                                                                                                  1538
                                                                                                                                                                                                                                    1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
CLONE: CD40-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                   714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   654
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                                                                                                                                                                                                                                                                                                                                   FILING DATE: O CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                    gttgtctatgttgaggcccactacgctcctttcccgtaagttctcgccttt 1708
                                                                                                                                                                                                                           cgcaatgtgccccgcgacactgttgagatctggcgacttgagaacaactccaacggttgg 153
TTTCCCATTTTCAAGCATTACCAAGTTGCTTTTCATGGTATAATATCCTTT 424
                                                                 AGAGCAGAAGGTGACTTGAGTGTAGACATAATAGAGTCCTTCTCTTTTAACCGTCAGCTG
                                                                                                                                                             actcaccctgttcacattcacctcgttgacttccgagtcctttctcgttccactgcccgt 159
                                                                                                                                                                                                                                                                 GACAAACACAGAAGCACCAGCTTGTAATTCAAACACTCCGCCCAAGTGAACAGACTGCTG 655
                                                                                             CTCGCAAAGCTGGGAAGCTGTGGGTATTTGCCGCCTTGAGTAAGATTCTCTCAGATCC
                                                                                                                                 ACTGCTGGGCTTCAGCCAGAGGCCGACGATGAATGGGCGTTGACTCGAAGGCTCCCGATT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perkins, Patricia
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r 23, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.2; D
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 198;
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Search completed: October Job time: 8530 sec

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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on:
  score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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		ASO_TOBAC	<u>ب</u>	578	4.5	139	42
		LAC1_EMENI	L	609	4.7	147.5	41
		LAC3_TRAVI	۳	473	4.9	151.5	40
9 saccharomyc		YD56_YEAST	Ц	608	5.1	160	39
		LAC2_AGABI	μ	520	5.1	160	38
l agaricus bi		LAC1_AGABI	<u>سر</u>	520	5.3	165	37
4 cucurbita p		ASO_CUCPM	<u>_</u>	552	5.3	166	36
8 trametes ve	Q12718	LAC2_TRAVE	ш	519	5.4	167	35
2 escherichia	Q4745	PCOA_ECOLI	_	605	5.5	172.5	34

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EMBL; AB007638; BAA22774.1; ALT_INIT.
EMBL; AB007638; BAA22774.1; --
EMBL; X05678; CAA29165.1; ALT_INIT.
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Sandman K., Kroos L., Cutting S.M., Youngman P., Losick R.;
"Identification of the promoter for a spore coat protein gene in
Bacillus subtilis and studies on the regulation of its induction
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Donovan W., Zheng L., Sandman K., Losick R.;
"Genes encoding spore coat polypeptides from
J. Mol. Biol. 196:1-10(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis of the groESL-cotA region of the Baci genome, containing the restriction/modification system pun Res. 4:335-339(1997).
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Phenoxazinone synthase (EC 1.-.-.) (PHS).
                                                                                                                                                                                                                          SUBUNITS
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J. Bacteriol. 177:5740-5747(1995).
                                                                                                                                                                                                                                                              "Nucleotide sequence, transcriptional analysis, and glucose regulation of the phenoxazinone synthase gene (phsA) from
                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacte
Actinomycetales; Streptomycineae;
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STRAIN+K12 / W3110;
STRAIN+K12 / W3110;
MEDLINE-94261430; PubMed-8202364;
Fujita N., Mori H., Yura T., Ishihama A.;
Fujita N., mori H., Yura T., Ishihama A.;
Fuystematic sequencing of the Escherichia coli
the 2.4-4.1 min (110,917-193,643 bp) region.";
the 2.4-4.1 min (20,917-193,643 bp) region.";
                                                                                                                                                                                                                                                    Electrophoresis 20:2181-2195(1999).

- COFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARIT 19 SUBCELLULAR LOCATION: Periplasmic (Potential).

- I SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

- I SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
EcoGene; EG12318; yacK.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2
                                              EMBL; D26562; CAB20297.1; ALT_FRAME. EMBL; AE000121; AAC73234.1; -. PIR; S45200; S45200.
                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Link A:J., Robison K., Church G.M.;
"Comparing the predicted and observed properties
in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
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STRAIN=K12 / EMG2
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Riley M., Collado-Vides J., Glasner J.D., Rode C.K., I
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Matches 131
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MEDLINE=97443975; PubMed=9298646;
Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties of a comparing the predicted and observed properties of a comparing the predicted and observed properties of a comparing the product of the genome of Escherichia coli K-12.";

In the genom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Periplasmic; Signal; Complete proteome.
SIGNAL
1
27
CHAIN
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470
DOMAIN
68
164
PLASTOCYAN
SEQUENCE 470 AA; 51858 MW; C843A5Av
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M63491; AAA24398.1;
PIR; S20461; S20461.
EccoGene; EG11376; sufI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of the Escherichia coli gene for 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC)."; Mol. Gen. Genet. 232:295-303(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001117; Cu-oxidase
Pfam; PF00394; Cu-oxidase; 1.
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MEDLINE=97426617; PubMed=9278503;
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nce 277:1453-1474(1997).
QPWPMLNVQPRKYRFRFLNAAVSRSFALYLATSEDSETRLPFQVIAADGGLLEGPVDTDT
                                              LAGMWLVEDEVSKSLPIPNHYGVDDFPVIIQDKRLDNFGTPEYNEPGSGGFVGDTLLVNG
                                                                                            QAGVYMIQDPAEDALNLPSGYGEFDIPLVLTAKRYNADGTLFSTNGEVSSFWGDVIQVNG
                                                                                                                                                                                              SPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYYYPNRQAARMLWYHDHAMSITAENAYMG
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67; Mismatches
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PLASTOCYANIN-LIKE.
; C843A5A4CB146688
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2.5e-15;
les 205;
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P40799;
01-FEB-1995
                                                                                                                                        Quail M., Whitehead
                                                                                                                                                               Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
                          -!- SUBCELLULAR LOCATION: I
-!- SIMILARITY: CONTAINS 1
-!- CAUTION: Ref.1 sequence
                                                                                                             "Complete genome sequence of a multiple enterica serovar Typhi CT18.";
                                                                                                                                                    Krogh A., Larsen T.S., Leather S., Moule S., O'Gao
Quail M., Rutherford K., Simmonds M., Skelton J.,
                                                                                                                                                                                                                                                                                                                                                                McClelland M., Sanderson K.E., Spieth J., Clifton Courtney L., Porwollik S., Ali J., Dante M., Du F. Leonard S., Nguyen C., Scott K., Holmes A., Grewal Ryan E., Sun H., Florea L., Miller W., Stoneking T
                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-S.typhimurium; STRAIN-LT2 / MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cong J., Schmid M.B.; Submitted (APR-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhimurium, Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein sufI precursor.
SUFI OR STM3172 OR STY3349.
                                                                                 Nature 413:848-852(2001).
                                                                                                                                                                                                                                                    SPECIES=S.typhi; STRAIN=CT18; MEDLINE=21534947; PubMed=11677608;
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence
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schmid M.B.;
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                           Ref.1 sequence
                                                                                                                                        Barrell B.G.;
             in position 413.
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Last sequence
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P43561;
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01-NOV-1995 (Rel.
16-OCT-2001 (Rel.
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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EMBL; AE008845; AAL22046.1;
EMBL; AL627277; CAD03004.1;
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                                                                                                                                                                                                                                                                                           QPWPMLNVQPRKYRFRFLNAAVSRSFALYLATSEDSETRLPFQVIAADGGLLEGPVDTDT
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                                                                                                                                                                                                                                                                                                                                                 ENVSMTVAGLLVPGPLMGGPARMMSPNADWAPVLPIRQSAATLWYHANTPNRTAQQVYNG
                                                                                                                                                                                                                                                                                                                                                                                                                          ASGIALCAGAIPLRANAAGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALGLAVIGGSSVDARSVAGRSTDMPSGLTKRQTQLSPPLALYEVPLPIPPLKAPNTVPNP
                                                                                                                                          RGVEPY-EAAGLKDVVWL---ARREVVYVEAHYAPFP
                                                                                                                                                                                                                                     LSLAPGERREILVDMTNGDEVSITCGEAASIVDRIRGFFEPSSILVSTLVLTLRP----T
                                                                                                                                                                                                                                                                        AQSPYVEVSRGWVRLRLLNASNSRRYQLQMSDGR-----ALHVISGDQGFLPAPVSVKQ
                                                                                                                                                                                                                                                                                                             LAGMWLVEDDISKTLPIPNHYGVDDFPVIIQDKRLDNFGTPEYSEPGSGGFVGDTLLVNG
                                                                                                                                                                                                                                                                                                                                                                                                      NTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSPGPTIIVPRGTESVVRFVNSGENT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
68
470 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                          STANDARD;
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470
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, Last sequence upon Last annotation of Copper oxidase FET
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        (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 310; DB 1;
Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLASTOCYANIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
PROTEIN SUFI.
                                                                          PRT;
 Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61E84D4D42B025FB CRC64;
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                           FET5 precursor
                                             update)
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 Saccharomycetes
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A Spizzo T., Byersdorfer C., Duesterhoeft S., Eide D.;

"The yeast FET5 gene encodes a FET3-related multicopper oxidase
T implicated in iron transport.";

L Mol. Gen. Genet. 256:547-556(1997).

C -!- FUNCTION: IRON TRANSPORT MULTICOPPER OXIDASE, WHICH IS REQUIRED
FOR FERROUS IRON HIGH AFFINITY UPTAKE. MAY BE REQUIRED TO OXIDIZE
C FE(II) AND RELEASE IT FROM THE TRANSPORTER. ESSENTIAL COMPONENT C
COPPER-DEPENDENT IRON TRANSPORT;
C COPACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH
C CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

C -!- SIMILARITY: BELONGS TO THE MULTICOPPER OXIDASE FAMILY.

-!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama Yamazaki M., Tashiro H., Eki T.; Yamazaki M., Tashiro H., Eki T.; Tanalysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001117; Cu-oxidase.
InterPro; IPR00335; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D50617; BAA09
EMBL; D44598; BAA08
HSSP; P37064; 1AOZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib;ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95400292; PubMed=7670463;
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NCBI_TaxID=4932;
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080; MULTICOPPER_OXIDASE2; 1.
Transmembrane; Signal; Transport;
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 Saccharomycetaceae;
                                                                                        COPPER (TYPE 2)
COPPER (TYPE 3)
COPPER (TYPE 3)
COPPER (TYPE 3)
COPPER (TYPE 1)
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COPPER (TYPE 1)
COPPER (TYPE 1)
                                                     N-LINKED (GLCNAC.
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PLASTOCYANIN-LIKE 2
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(GLCNAC.)
(GLCNAC.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                      (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                  MULTICOPPER OXIDASE FET5
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Matches
SEQUENCE FROM N.A.

STRAIN-RD / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed=7542800;

MEDLINE-95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A.

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.

McKenney K., Sutton G., Fitzhugh W., Fields C.A., G

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelle
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01-NOV-1995 (Rel. 32, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                               Protein sufI homolog SUFI OR HI0733.
                                                                                                                                                                                                           P44847;
                                                                                                                                                                                                                                  _HAEIN
                                                                                                             Haemophilus
                                                                                                                       Bacteria;
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22.3%;
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red. No. 4.2e
Mismatches
                                                                                                                       subdivision;
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                       Clayton R.A., Kirkness
Dougherty B.A., Merrick
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  Kelley
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AC QO
AC QO
DT 01
DT 15
DT 15
DE La
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Best Local S
Matches 96
 parasitica).
Eukaryota; Fungi
Diaporthales; Va.
NCBI_TaxID=5116;
                                                                                                                     LAC1_CRYPA
Q03966;
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                            CRYPA
                                                    Cryphonectria
                                                                  (Urishiol oxidase) LAC-1.
                                                                                            Laccase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               influenzae xu...

Science 269:496-512(1995).

-!- SUBCELLULAR LOCATION: Periplasmic (Potential).

-!- SIMILARITY: STRONG, TO E.COLI AND S.TYPHIMURIUM.

-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.

-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                        15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U32756; AAC22390.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Periplasmic; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR;
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                                                                                                                                                                                                                                                                                  LDVARGWIRLRLLNASLARAYDLRL---DNDQEMLL----IAQDLGFLPKAKSVKSLVLSP
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            Fungi; Ascomy
es; Valsaceae;
                                                                                                        (Rel.
                                                                                                                     (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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68
                                                   parasitica
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                                                                                                                                                              STANDARD;
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                                                                                          35, Created)
35, Last sequ
36, Last anno
(EC 1.10.3.2)
                           Ascomycota;
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311
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                                                                                         Last sequence update)
Last annotation update)
1.10.3.2) (Benzenediol:oxygen
             Cryphonectria
                                                   (Chesnut
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BY SIMILARITY.
BY SIMILARITY.
PROTEIN SUFI HOMOLOG.
PLASTOCYANIN-LIKE.
PLASTOCYANIN-LIKE.
W; 436173F59F1E1772 CRC64;
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Pred.
                           Pezizomycotina;
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                                                   blight
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.8e-10;
                                                   fungus)
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                          Sordariomycetes
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                                                   (Endothia
                                                                                            oxidoreductase)
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Best Local Sim
Matches 155;
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EMBL; S38903;
HSSP; P37064;
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CARBOHYD
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CARBOHYD
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CARBOHYD
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METAL
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InterPro; IPR002355; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1;
PROSITE; PS00080; MULTICOPPER_OXIDASE2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wall modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi G.H., Larson T.G., Nuss D.L.;
"Molecular analysis of the laccase gene
fungus|and selective suppression of its
hypovirulent strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
MEDLINE=92314427; PubMed=1535523;
                                                                                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase;
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  74
                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted (Potential).
SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR: BINDS 4 CU-IONS PER MOLECULE. CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
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                     SGLIASQLSWAAPSLLH-
                                         SGLTKRQTQLSPPLALYEVPLPIPPLKAPN-----
                                                             Conservative
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591
189
356
356
126
128
171
171
                                                                       7.0%;
                                                                                                                  64696 MW;
                                                                                                                                                                                                                                                                                                                                                                                       Copper; Metal-binding; Lignin degradation;
                    PLEPRQQPNCNTASNRACWISGSYDITTDYEVKTPLTGV
                                                             78;
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N-LINKED
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COPPER
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COPPER
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PLASTOCYANIN-LIKE
PLASTOCYANIN-LIKE
                                                                                Score
                                                                                                                                                                            N-LINKED
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                                                                                                                                                                                                 COPPER
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                  B2F44CB2AAD77701
                                                             Mismatches
                                                                       No. 3.
                                                                                                                                                                                                                                                                               TYPE (TYPE)
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                                                                                                                                                                            (GLCNAC.
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FET3_CANAL
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P78591;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
                                This
                                                                                                         DEPENDENT IRON TRANSPORT (BY SIMILARITY).

-i- COFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WI-
CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TO
2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY)
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL SURFACE I
                                                                                                                                                                                        Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: IRON TRANSPORT MULTICOPPER FERROXIDASE REQUIRED FOR FERROXS IRON HIGH AFFIXITY UPTAKE. REQUIRED TO OXIDIZE FE(II) RELEASE IT FROM THE TRANSPORTER: ESSENTIAL COMPONENT OF COPPEI
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; ,
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                  FET3
                                                                                                                                                                                                                                                                                                                                                                                              Iron
                                                                                                                                                                                                                                                                                                                                                                Candida albicans (Yeast).
                                                                                                                                                                                                                                                                       STRAIN=1161;
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5476;
                                                                                                                                                                                                                                                        Hundt S.,
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544
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SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restric
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el. 35, Last annotation
multicopper oxidase pre
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                                                            TO THE MULTICOPPER OXIDASE FAMILY S 3 PLASTOCYANIN-LIKE DOMAINS.
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InterPro; IPR002355; Multi
Pfam; PF00394; Cu-oxidase;
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                                               DTDTLYISMAERWEVVI-----DFSTFAGQSIDIRNLPGADGLGVEPEFDNTDKVMRFV
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                                                                                                                                                                                                                                                                            PDGVYPRKMIGENDSWPLPTLRVKKGDRVQLYLINGEDNLN-TTLHFHGLEVRGANQMDG
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                              -TDLIYITVAQRYGVLITTKNSTDKNYVFMNGVDTTML---DSVPADLQVNGTNYI--
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01-NOV-1997
15-JUL-1999
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between
the Euro
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphyllophorales; Coriolaceae; Trametes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAC5_TRAVE Q12717;
              DOMAIN
DOMAIN
DOMAIN
METAL
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SIGNAL
                                                                                                  PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG
Oxidoreductase; Signal; Copper; Metal-binding; Gl;
                                                                                                                                         InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
                                                                                                                                                                                                                   use by non-profit institutions as low-
modified and this statement is not remov-
entitles requires a license agreement (s)
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Aphyllophorales; NCBI_TaxID=5325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NoV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Laccase 5 precursor (EC 1.10.3.2) (Benzenediol:oxygen (Urishiol oxidase) (Diphenol oxidase) (Laccase IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRAVE
                                                                                                                                                                               EMBL; U44431; AAC49829.1; HSSP; P37064; 1AOZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and sequence analysis of two laccase complementary DNAs the ligninolytic basidiomycete Trametes versicolor."; Gene 196:113-119(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ong
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Ong E., Pollock W.
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COFACTOR:
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                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: LIGNIN DEGRADATION AND PRODUCTS (PROBABLE).
CATALYTIC ACTIVITY: 4 benzenediol
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SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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3 OR COUPLED BINUCLEAR (
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                                                                                          degradation;
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7 (Rel. 35,
9 (Rel. 38,
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.B., Smith M.;
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498
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                                                                                         Multigene
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POTENTIAL.
LACCASE 5.
PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 2.
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COPPER (TYPE 3) (BY S
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                                                                                                           DFHLD---
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                                                                                                                                                                                        HPVHIHLVDFRVLSRSTARGVEPYEAAGLKDVVWLARREVVYVEAHYAPFPGVYMLHCHN
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This SWISS-PROT entry is copyright. It is produced through a clother the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thanatephorus cucumeris (Black scurf of potato) (Rhizoctonia solani). Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiales; mitosporic Ceratobasidiaceae; Rhizoctonia.
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Laccase 4 precursor (EC 1.10.3.2) (Benzenediol:oxygen
                                                                                                                                                                                                                SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: IN MYCELIA,
                                                                                                                                                                                                                                                                                                                 H(2)O.
COFACTOR: BINDS
                                                                                                                                                          SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                   CENTERS
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                                                                                                                                                                                                    LCC3
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                                                                                                                                                        BELONGS TO CONTAINS 3
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Xu F., Brown K.
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                                                                                                                                                          THE FAMILY OF MULTICOPPER PLASTOCYANIN-LIKE DOMAINS.
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InterPro: IPR001117; Cu-oxidase.
InterPro: IPR002355; MultiCu_oxidse2.
pfam; PF00394; Cu-oxidase; 3:
PROSITE; PS00079; MULTICOPPER_OXIDASE1;
PROSITE; PS00080; MULTICOPPER_OXIDASE2;
Oxidoreductase; Signal; Copper; Metal-bi EMBL; Z54277; CAA91042.1; degradation; 20 23 384 83 83 128 83 128 130 130 432 432 481 481 109 186 231 231 280 280 119 nal; Copper; Multigene f ı LACCASE 4.
PLASTOCYANIN-LIKE
PLASTOCYANIN-LIKE
PLASTOCYANIN-LIKE _OXIDASE1; FALSE_NEG.
_OXIDASE2; FALSE_NEG.
r; Metal-binding; Glycoprotein;
family; Polymorphism. (TYPE CYT) A CYTYPE CYT GLCNAC.
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                                                                                                                                                Schizosaccharomycetales; Schizosaccharomyces.
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                                                                   Submitted (NOV-1995) to
                                                                                       Murphy L., Niblett D., Harris D.,
                                                                                                    STRAIN=972;
                                                                                                                SEQUENCE FROM N.A
                                                                                                                                    NCBI_TaxID=4896;
                                                                                                                                                                        Eukaryota; Fungi; Ascomycota;
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         FUNCTION: COULD BE A IRON TRANSPORT MULTICOPPER OXIDASE, WHICH I REQUIRED FOR FERROUS IRON HIGH AFFINITY UPTAKE. MAY BE REQUIRED OXIDIZE FE(II) AND RELEASE IT FROM THE TRANSPORTER. ESSENTIAL COMPONENT OF COPPER-DEPENDENT IRON TRANSPORT (BY SIMILARITY). COFFORTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH
                                                                                                                                                                                                                                                                                                                                            HYAPFPGVYMLHCH 502
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(Tel. 35, Cast annotation
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-NALEEPYDYDE-EYIISMTDWYYTPFNILVPDEFKT----

WKN--PTGAEPVPDTG

195

YMDGVPQSTQCEIPPGATFYYNYTALQNG-TYWYHSHDMSQYPD

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FDGWAEDTTQ----PGEYKDYYYPNRQAARMLWYHDHAMSITAENAYMGQAGVYMIQDPA

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InterPro; IPR002355; MultiCu_oxidse2.
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European Bioinformatics Institute
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rical protein; Glycoprotein; Transmuctase; Conner. Pro-
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Laccase 1 precursor (EC 1.10.3.2) (Benzenediol:oxygen (Urishiol oxidase) (Diphenol oxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Mycelium;
MEDLINE-97076915; PubMed-8975613;
                                              This
                                                                                                                                                                                                                                                                                 Appl. Environ. Microbiol. 62:834-841(1996).
-- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION
-- PRODUCTS (PROBABLE).
-- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenediol
                                                                                                                                                                                                                                                                                                                                                                                               Yaver D.S., Xu F., Golightly E.J., Brown K.M., Brown S.H., Rey M.W., Schneider P., Halkier T., Mondorf K., Dalboge H.; "Purification, characterization, molecular cloning, and exp "Purification, characterization, molecular cloning, and exp two laccase genes from the white rot basidiomycete Trametes
  the
                                                                                                                                                                                                                                                                                                                                                                                villosa
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Aphyllophorales; (
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COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTERNACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTERNACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTERNACTOR AND ADDRESS OF COUPLED BINUCLEAR (BY SIMILARITY).

SUBCULT: HOMODIMER.

SUBCELLULAR LOCATION: Secreted.

SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER 
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                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
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; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Coriolaceae; Trametes.
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~inding; Glycoprotein; F
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STANDARD; PRT; 529 AA.
Q12729;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 35, Last sequence update)
Laccase 1 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Diphenol oxidase).
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EMBL; Z22591; CAA80
HSSP; P37064; 1AOZ.
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Appl. Environ. Microbiol. 61:2408-241
-i- FUNCTION: LIGNIN DEGRADATION AND
PRODUCTS (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-FLORIDA; TISSUE-Mycelium;
MEDLINE-95314294; PubMed-7793961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pleurotus ostreatus (Oyster mushroom) (White-rot Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Fagaricales; Pleurotaceae; Pleurotus.
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basidiomycete Pleurotus ostreatus.";
Appl. Environ. Microbiol. 61:2408-2413(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sannia G.
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CATALYTIC ACTIVITY: 4 benzenediol +
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                                                             KDVVWLARREVVYVEAHY-APFPGVYMLHCH
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Search completed: October 3, 2002, 11:02:16 Job time: 440 sec

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Q93f57 pseudomonas	O24044 liriodendro	Q96wm9 botrytis ci	Q9hdq0 trametes tr		S	Q96wt3 candida gla	Q989b7 rhizobium l	Q12571 basidiomyce	Q9aui6 pinus taeda	Q9uvq5 marasmius q	Q9pa43 xylella fas	Q9c497 glomerella	Q941x2 oryza sativ	Q9y782 coprinus ci	Q93f47 pseudomonas		Q9c1z1 pichia past	ס	Q9aui2 pinus taeda	Q9fjd5 arabidopsis	6 rhizobium		Q96wnO botrytis ci	Q9kjb8 marinomonas	053858 mycobacteri	0		Q9hxm7 pseudomonas

ALIGNMENTS

RESULT Q9P8C3

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66 PAYTLFQAPLSIPPVKEPLFTVTNPYNGGEIDYYEIEIKHFSEQVFPDLGPADLVGYDGI 125	46 PPLALYEVPLPIPPLKAP-NTVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGM 104	6 ALRALALYLSIKGAQAMPKFELDIPEEEAAALAAIVEDDPANDLQRRSPANDLQRRSPLS 65	DARSVAGRSTDMPSGI	Matches 352; Conservative 83; Mismatches 131; Indels 34; Gaps 7;	58.7%; Score 1829;	SEQUENCE 602 AA; 66920 MW; 0303D991405228A3 CRC64;	62 602 PC			Appi. Environ. Microbiol. 67:2610-2616(2001). EMBL; AJ271104; CAB75422.1;	expression in Aspergillus awamori.";	"Cloning of a phenol oxidase gene from Acremonium murorum and its	Gouka R.J., van der Heiden M., Swarthoff T., Verrips C.T.;	MEDLINE=21268855; PubMed=11375170;	STRAIN=CBS 157.72	SEQUENCE FROM N.A.	[1]	нуростеатеs; нуростеасеае; mitosporic Hypocreaceae; Acremonium. NCHT TayTD=4578.	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	Acremonium murorum.	PPOA.	OT-DEC-2001 (ILEMBLICI. 19, LAST ANNOLATION UPGATE)	(TrEMBLrel. 15, Last	01-OCT-2000 (TrEMBLrel. 15, Created)	Q9P8C3;	Q9P8C3 PRELIMINARY; PRT; 602 AA.

pasteurella

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RESULT
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Q93M03;
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Streptomyces aureofaciens.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Streptomycetaceae; St
                                                                                                                                                                                                                                             Kormanec J., Bistakova J., Novakova R., Homerova D., Rei
"Cloning and characterization of a new polyketide gene of
streptomyces aureofaciens CCM3239.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AY033994; AAK61713.1; ...
SEQUENCE 475 AA; 52602 MW; AZED9A4C638DD0C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TIEMBLIEL 19, 01-DEC-2001 (TIEMBLIEL 19, 01-DEC-2001 (TIEMBLIEL 19, OXIDOREDUCTASE-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae; NCBI_TaxID=1894;
                                                                                                                                                                                                                                                                                                                                  STRAIN=CCM3239;
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NT---AVHLHGAHVLSEHDGLPMDTIVPGGERTYRYPNNQPAASLWYHDHAHHLEAENVF
                                                                      PNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSPGPTIIVPRGTESVVRFVNSGE- 127
                                                                                                               MAAAGGAAALFPWDRLTGAG-SQAVASSLA---TAEAAPIVPFAHAMPLP----KNLKPT 52
                                                                                                                                          LAVIGGSSV----DARSVAGRSTDMPSGLTKRQTQLSPPLALYEVPLPIPPLKAPNTVPN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVLPDYGYNSTALADPMQDEFRAKPYVDNDVEVRENAFSTDEIEAQVQLMASYLPYDNPD 598
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                           NTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYYYPNRQAARMLWYHDHAMSITAENAY 187
                                                      SFTATSDL-YEIRMQEAQVEIVKGL-MSKVRTYDGTFPGPTIRATQGREVVVRQINELQV 110
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                                                                                                                                                                                      19.2%; Score 599; 34.7%; Pred. No. 5
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Best Local S
Matches 177
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; AP002860; Bab18287.1;
InterPro; IPR002355; MultiCu_oxidse2.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9FTS3 PRELIMINARY; PRT; 637 AA. O9FTS3; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) PUTATIVE SPORE COAT PROTEIN-LIKE PROTEIN. P0409B08.14.
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SEQUENCE 63
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Sasaki T., Matsumoto T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
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FAWFTRDFAENGSTWTRKTYTYPNVQAPGNLWYHDHALGLTRVSLLAGLLAAYVIEKPEL
                                                                                                                                                              PTIIVPRGTESVVRFVN------SGENTSPNSVHLHGSFSRAPFDGWA
                                                                                                                                                                                                                                                                                                                                   SVISKSRWGWASDDPN-----DDEYTPP----DHPLPAPAAGRRRWPVM---TSLNLTKY 104
                                                                                                                                                                                                                                                                                                                                                                                       SYDARSVAGRSTDMPSGLTKRQTQLSPPLALYEVPLPIP-----PLKAPNTVPNPNTG
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                                                                                                          PTIVARQGVPLAVEWQNHLPDAHILPWDPKVPTAIPKKGGVPTVVHLHGGAHPPEFDGHA
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                                                   ----EDTTQPGE---YKDYYYPNRQAARMLWYHDHAMSITAENAYMGQAGVYMIQDP-A
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28.7%; Pred. No. 1.3e-
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Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               023123;
01-JAN-1998 (TrEMBLrel. (
01-JAN-1998 (TrEMBLrel. (
01-DEC-2001 (TrEMBLrel. ;
F19G10.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. COLUMBIA;
Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Oji O., Osbozne B.I., Shinn P., Sun H., Toriumi M., Vyotskai Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AR000657; AAB72167.1; -.
InterPro; IPR001117; Cu-oxidase.
Pfam; PF00394; Cu-oxidase; 1.
SEGUENCE 568 AA; 64355 MW; C4314C889576E35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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  169
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                                       YYYPNRQAARMLWYHDHAMSITAENAYMGQAGVYMIQDPA-EDALNLPSGYGEFDIPLVL
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LHYENKQQPGNMWYHDHAMGLTRVNLLAGLVGAYILRHHAVESPFQLPTG-DEFDRPLII 227
                                                                                                     PKSHILPWDPTISPATPKHGGIPTVVHLHGGIHEPTSDGNADAWFTAGFRETGPKWTKTT
                                                                                                                                                                                                             IKPASLQIGMESTKWKFHRDL-PATPVFAYGTSRSKATVPGPTIETVYGVDTYVTWRNHL 108
                                                                                                                                                                                                                                                             IRPESHQI-----YPDLEPANMYGYDGMS-----PGPTIIVPRGTESVVREVNSG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVYHCHILDHEDNAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCNLDQHAVGPVVPVPEEEKTWKNAVKIPPEFMTSVVVAFRLVEANQPYPFDATTEPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VTETPKSGTTELWQV-INLTGDNHPLHLHIATFQAIKMTKIEGFQVFKDCMIKNNNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMPDKSKVPEH--GVPYASVAALPPPTTTRYIVLYENQT-----APGNLYINGLELEDP-499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESPDTSEVPANLRDVPFPEGGNWDPANPT-----DDETFTFGRANGQWTINGVTFSDVE
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                                                                                                                                                                                                                                                                                                                        154;
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                                                                                                                                                                                                                                                                                                                           Conservative
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Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                     Score 489.5; DB 10
Pred. No. 8.3e-28;
7; Mismatches 181;
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Y.,
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                                                                                                                                  Query Match
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Matches 156; Conser
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01-JUN-2001
01-JUN-2001
01-DEC-2001
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Sasaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE SPORE COAT PROTEIN.
P0044F08.18 OR P0037C04.31.
                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2001) to the EMBL/GenBank/DDBJ EMBL; AP00.2909; BAB21188.1; -. EMBL; AP00.233; BAB55542.1; -. InterPro; IPR00.235; MultiCu_oxidse2. PROSITE; PS00.080; MULTICOPPER_OXIDASE2; UNKNOW PS00.080; MULTICOPPER_OXIDASE2; MULTICOPPER_OXIDASE2; UNKNOW PS00.080; MULTICOPPER_OXIDASE2; MULTICOPPER_OXIDASE2; MULTICOPPER_OXIDASE2; MULTICOPPER_OXIDASE2; MULTICOPPER_OXIDASE2; MULTICOPPER_OX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Oryza sativa nipponbare(GA3)
clone:P0037C04.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Oryza sativa nipponbare(GA3)
clone:P0044F08.";
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                                                                                                                                                                                                                                                                                                             Coat protein.
SEQUENCE 582 AA;
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                                                             QIYPDLEPANMVGYDGMS-----PGPTIIVPRGTESVVRFVN--
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NIPPONBARE;
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Matsumoto T.,
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ilarity 28.9%;
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/ta; Liliopsida; Poales;
                                                                                                                                      60;
                                                                                                                                  Score 476.5;
Pred. No. 7.8e
50; Mismatches
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hes 165;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence
01-JUN-2001 (TrEMBLrel. 17, Last annotati
PUTATIVE SPORE COAT PROTEIN-LIKE PROTEIN
P0409B08.12.
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002860; BAB18285.1; -. InterPro; IPR002355; MultiCu_oxidse2. PROSITE; PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, clone:P0409B08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                              -PNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMS-----PGPTIIVPRGTESV 119
                                                                                                                                                          SVDARSVAGRSTDMPSGLT----KRQTQLSPPLALYEVPLPIPPLKAPNTV------
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TWQFHRDMPPTPVFVY-GQSLQTATFPGPTIVARYNVPLY
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Last annotation update)
                                                                                                                                                                                                                                       Score 455.5; DB 10; Pred. No. 3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eptophyta; Embryophyta; Tracheophyta;
Liliopsida; Poales; Poaceae;
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RESULT
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                                      Sasaki.T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chr
clone:P0044F08.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
EMBL; AP002860; BAB18284.1; -.
EMBL; AP002909; BAB21194.1; -.
InterPro; IPR002355; Multicu_oxidse2.
                                                                                                                                                                                                                                                                                                                                             09FTS6;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE SPORE COAT PROTEIN-LIKE PROTEIN
P0409B08.11 OR P004F08.29.
Oryza sativa (Rice)
                                                                                                                                                                                                      "Oryza sativa nipponbare(GA3) genomic DNA, clone:P0409B08.";
                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
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              Coat protein
                       InterPro; IPR002355; multiCu_oxidse2
PROSITE; PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1.
                                                                                                                                        STRAIN=CV.
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                                                                                                                                                                                                                                  Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                       NCBI_TaxID=4530;
                                                                                                                                                          SEQUENCE FROM N.A.
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588 AA;
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Best Local Similarity
Matches 141; Conserv
                                                                                                                Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T. Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Shinozaki T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length cDNA of gene F23N20.3 (G1:12323429)."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                              EMBL; AY050818; AAK92753.1; -. Coat protein.
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Pred. No. 1e-24;
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, Palm C.J.,
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01-DEC-2001
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067206;
                                                                                                                                                                                                                                     MEDLINE=98196666; PubMed=9537320; Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox Deckert G., Warren P.V., Snead M.A., Keller M., Aujay M., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aqu
                                                                                                 Nature 392:353-358(1998).
EMBL; AE000724; AAC07157.1; -.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; Multicu_oxidse2.
Cell division; SEQUENCE 527
                                                                                                                                                                                                                    aeolicus
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Aquifex aeolicus
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                                                     Pfam; PF00394; Cu-oxidase; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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(TIEMBLrel. 19, Last annotation update)
CELL DIVISION PROTEIN (SUFI).
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Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Gill J.B., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.B., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Millitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;.

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Coat protein.
SEQUENCE 591 A
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                    SEQUENCE FROM N.A.

Lee I.S., Lim S.Y., Choi S.-Y.,
"cuiD, a gene encoding a multicopper cloning and characterization.";
                                                                                                                                               Salmonella.
NCBI_TaxID=602;
                                                                                                                                                                                                                                                       CUID.
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  Submitted
                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                             Salmonella
                                                                                                                                                                                                                                                                              MULTICOPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 408:816-820(2000).
EMBL; AC016972; AAG51692.1;
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                  "Complete genome structure of Mesorhizobium loti."; Mesorhizobium 10ti."; DNA Res. 7:331-338(2000).
EMBL; AP003002; BAB50448.1; -... InterPro; IPR001117; Cu-oxidas
                                                                                                                             Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato (Matanabe A., Idesawa K., Ishikawa A., Kawashina K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., I Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                      MEDLINE=21082930; PubMed=11214968;
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                 May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001). EMBL, AE006230; AAK04022.1; InterPro; IPR001117; Cu-oxidase. InterPro; IPR002355; MultiCu_oxidse2.
                                                                                                                                      MEDLINE=21145866; PubMed=11248100;
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         Corstjens P.L.A.M., de Vrind J.P.M., Goosen T., de Vrind-de Jong E.W.; "Identification and Molecular Analysis of the Leptothrix discophora SS-1 mofA Gene, a Gene Putatively Encoding a Manganese Oxidizing Protein with Copper Domains."; Geomicrobiol. J. 14:91-108(1997).
                                                                                                                                        STRAIN-SS-1
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                                                                                                                                                                                                                                                                                                                                                                       KTFKPEGRALKDVVNLRPYEKVIIRFKQGH----TGLKMYHCHILEHENLGMMGMFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                      ANGQWTINGVTFSDVENRLLRNVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSRSTAR
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58572 MW; 1665D9B6C7C6743F CRC64;
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Best Local :
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 Q9PME8;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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SIGNAL
                                               Q9PME8
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                                                                                                         EDTKPGYGPNTRTMMQIKVRAAITTP
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34 1662 PO7
1662 AA; 174293 MW;
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ilarity 19.4%;
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Pred. No. 2.
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Best Local Similarity 24.6
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
Nature 403:65-668(2000).
Nature 403:65-668(2000).
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001315; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
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STRAIN-NCTC 11168;
MEDLINE-20150912; PubMed-10688204;
MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Jugels K., Karlyshev A.V., Rutherford K.M., van Vliet A.H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome: Sequence 513 AA; 59076 MW; 019CBAE21B7A1555 CRC64;
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NCBI_TaxID=197;
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
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                                                                                                                                                                                                                                                   VVDEVLESPDT-----SEVPANLRDV-PFPEGGNWDPANPTDDETFTFGRAN- 404
                                                                                                 VDFRVLSRSTARGVEPYEAAGLKDVVWLARREVVYVEAHYAPFPGVYMLHCHNLIHEDHD 510
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MMGNLEV 511
                                                                   TQFELISSKLNGKVQKAEFRAFRDTINVRPNEELRLKMK-QDFKGLRMYHCHILEHEDLG 504
                                                                                                                                       SENELKIALASMFLINGKSYDLKRIDLSSKL-----GVVEDWIVINKSH-MDHPFHIHG 445
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ALIGNMENTS

FILE REFERENCE: GC584
CURRENT APPLICATION NUMBER: US/09/401,476
CURRENT FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 583
TYPE: PRT
ORGANISM: Stachybotrys chartarum
US-09-401-476-2 Sequence 2, Application US/09401476
Patent No. 6168936
GENERAL INFORMATION:
APPLICANT: Wang, Huaming
TITLE OF INVENTION: No. 6168936el Phenol Oxidizing
FILE REFERENCE: GC584 Query Match
Best Local Similarity WGDVIQVNGQPWPMLNVQPRKYRFRFLNAAVSRSFALYLATSEDSETRLPFQVIAADGGL RFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYYYPNRQAARMLWYHDHAMS KAPNTVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSPGPTIIVPRGTESVV KAPNTVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSPGPTIIVPRGTESVV RFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYYYPNRQAARMLWYHDHAMS 100.0%; ilarity 100.0%; Conservative 0; 0 Score 3114; DB 4; Pred. No. 3.3e-290;); Mismatches 0; Length 583; Indels 0; Gaps

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CURRENT FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                              GLLEGPVDTDTLYISMAERWEVVIDFSTFAGQSIDIRNLPGA-DGLGVEPEFDNTDKVMR 357
                                                                                                                                                                                                                                                                                                                                                                  MSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPLVLTAKRYNADGTLFSTNGEVS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDVVWLARREVVYVEAHYAPFPGVYMLHCHNLIHEDHDMMAAFNVTVLGDYGYNYTEFID 532
                                                                                      DYENRLLRNVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSRST---ARGVEPYEAAGL 472
                                                                                                                                                           FVVDEVLESPDTSEVPANLRDVPFPEGGNWDPANPTDD--ETFTFGRANGQWTINGVTFS 415
                                                                                                                                                                                                          GLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNLGGSIGGIGTDTDYDNTDKVMR 355
                                                                                                                                                                                                                                                                              SEWGDVIHVNGQPWPFKNVEPRKYRFRFLDAAVSRSFGLYFADTDAIDTRLPFKVIASDS 295
                                                                                                                                                                                                                                                                                                  SFWGDVIQVNGQPWPMLNVQPRKYRFRFLNAAVSRSFALYLATSEDSETRLPFQVIAADG 298
                                                                                                                                                                                                                                                                                                                                               MHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSKQYTANGNLVTTNGELN 235
                                                                                                                                                                                                                                                                                                                                                                                                                   VVRFINNAE--APNSVHLHGSFSRAAFDGWAEDITEPGSFKDYYYPNRQSARTLWYHDHA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                      VVRFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYYYPNRQAARMLWYHDHA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKAPN-TVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSPGPTIIVPRGTES 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLRNVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSRSTARGVEPYEAAGLKDVVWLAR 480
                                                                  DVQNRLLANVPVGTVERWELINAGNGWTHPIHIHLVDFKVISRTSGNNARTVMPYE-SGL 466
                                                                                                                                      FVVADDTTQPDTSVVPANLRDVPFP-----SPTTNTPRQFRFGRTGPTWTINGVAFA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MFKHTLGAAALSL-LFNSNAVQASPVP--ETSPATGHLFKRVAQISPQYPMFTVPLPIPP 57
KDVVWLGRRETVVVEAHYAPFPGVYMFHCHNLIHEDHDMMAAFNATVLPDYGYNATVFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPFLLGEFENGSGDFSELAITDRIQEMASFNPYAQADDDAAEE
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US-08-749-882A-2
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,
FILING DATE: 15-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 616 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Purified Scytalidium Laccases
TITLE OF INVENTION: And Nucleric Acids Encoding Sa
NUMBER OF SEQUENCES: 9
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                  279
                                                    228
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                                                                                                                                                                                                                 118 SVVRFVNSGENTSPNSVHLHGSFSRAP-----FDGWAEDTTQPGEYKDYYYPNRQAARML 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                   74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lambiris, Elias REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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                                                                                TLFSTNGEVSSFWGDVIQVNGQ-----
                                                                                                                                                WYHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPL-VLTAKRY---NADG 228
                 LATSEDSETRLPFQVIAADGGLLEGPVD---TDTLYISMAERWEVVIDFS
                                             LVIETLAKGNAPFSDNVLINGTAKHPTTGEGEYAIVKLTPDKRHRLRLINMSVENHFQVS
                                                                                                                  WYHSH-FSAQYGN---GVSGAIQINGPA----SLP-----YDIDLGVLPLQDWYYKSADQ 227
                                                                                                                                                                                                                                                 PNTG------VVRRYTFDI---TEVDNRPGPDGVIKEKLMLINDKLLGPTVFANWG-D 121
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25.2%;
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Pred. No. 9.8e-16;
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 Query Match
Best Local Similarity
Matches 137; Conserv
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                                                                                                                                                                                                TELEPAX: 214-07 TELEPAX: 210-07 INO: 2
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE 616 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                      SUPTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,134
FILING DATE: 04-CCT-1995
CLASSIFICATION: 435
ATTORNEY ACCOUNTY
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                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 212-878-9652
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                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: NO. 58437450 No. 5843745disk Of No. 5843745th Amer#ca,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                             NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33
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STATE: NY
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And Nucleric Acids Encoding Same
: 9
                8.2%;
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Score 254.5;
Pred. No. 9.8e
71; Mismatches
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es 171;
                                 DB 2;
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Indels 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08991531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                 ATTORNEY/AGENT INFORMATION: NAME: Rozek, Carol
                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cherry, Joel
TITLE OF INVENTION: Myc
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                             COMPUTER: IBM CONTROL OPERATING SYSTEM:
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CITY: New York
                                                     CLASSIFICATION:
                                                                                                                                                                                                                          COUNTRY: UZIP: 10174
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REGISTRATION NUMBER:
                                                                     APPLICATION NUMBER: US/0
FILING DATE: 16-DEC-1997
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US-09-032-315-9

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Best Local
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                                                                                                                                                          GENERAL INFORMATION:
                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59858180 No.
                                                                                  APPLICANT: Svendsen, Allan APPLICANT: Xu, Feng TITLE OF INVENTION: LACCASI NUMBER OF SEQUENCES: 10
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TELECOMMUNICATION INFORMATION: 212-867-0123
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CITY:
STATE:
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TOPOLOGY: 15
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                                    405 Lexington Avenue
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25.2%; Pred. No. 1.2e
tive 70; Mismatches
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Best Local S
Matches 137
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MEDIUM TYPE: Diskett
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ZIP: 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 27-FE
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SOFTWARE: FastSE(
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IAXH 558
                                                                                                                                                                                                                                              NLRDVP----FPEGGNWDPANPTDDE-----TFTFGRANGQWTINGVTFSDVE-----
                                                                                                                                                                                                                                                                                                                      TFAGQS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WYHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPL-VLTAKRY---NADG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNTG-----VVRRYTFDI---TEVDNRPGPDGVIKEKLMLINDKLLGPTVFANWG-D 121
                                                                    SPDSETRFVFDPAVDLPRLRGHNPVR---
                                                                                                                                        YVMNNDLSSIPVKNNIVRVDGVNEWTYWLVENDPEGRLSLPHPMHLHGHDFFVLGRSPDV
                                                                                                                                                                          ---NRLLRNVP--RDTVEI-----WRLENNSNG---WTHPVHIHLVDFRVLSRS---
                                                                                                                                                                                                             VQKNVPVDGFVKEPGNTLPVTLHVDQAAAPHVFT-----WKING-SAADVDWDRPVLE
                                                                                                                                                                                                                                                                                 TFGGQQKCGFSHNPAPAAIFRYEGAPDALPTDPGAAPKD-----HQCLDTLDLS--PV
                                                                                                                                                                                                                                                                                                                                                         LA------KHTMTVIAAD----MVPVNAMTVDSLFMAVGQRYDVTIDASQAVGNYWFNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLFSTNGEVSSFWGDVIQVNGQ------PWPMLNVQP-RKYRFRFLNAAVSRSFALY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVVRFVNSGENTSPNSVHLHGSFSRAP-----FDGWAEDTTQPGEYKDYYYPNRQAARML
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27-FEB-1998
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                                                                                                     --TARGVEPYEAAGLKDVVWLARREVVYVEAHYAPFPGVYMLHCH
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Pred. No. 1.
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hes 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 137;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 50.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: No. 59983530 No.
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                                                                                                                                                                                                                                                         173
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                                                                                                                                                                                                                                                                                           122 TIEVTVNNHLRTNGTSIHWHGLHQKGTNYHDGANGVTECPIPPGGSRVYSFRARQYGTS: 180
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                     69 PNTGEDILYYEMEIRPESHQIYPDLEPANMVGYDGMSP------GPTIIVPRGTE 117
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                                TFAGQS-----IDIRNLPGA-DGLGVEPEFDNTDKVMRFVVDEVLESPDTSEVPA 374
                                                                                                         LATSEDSETRLPFQVIAADGGLLEGPVD---TDTLYISMAERWEVVIDFS------
                                                                                                                                             LVIETLXKGNAPFSDNVLINGTAKHPTTGEGEYAIVKLTPDKRHRLRLINMSVENHFQVS 287
                                                                                                                                                                                                                  WYHSH-FSAQYGN---GVSGAIQINGPA----SLP----YDIDLGVLPLXDWYYKSADQ 227
                                                                                                                                                                                                                                                       WYHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPL-VLTAKRY---NADO 228
                                                                                                                                                                                                                                                                                                                            SVVRFVNSGENTSPNSVHLHGSFSRAP----FDGWAEDTTQPGEYKDYYYPNRQAARML 172
                                                                                                                                                                                                                                                                                                                                                          PNTG------VVRRYTFDI---TEVDNRPGPDGVIKEKLMLINDKLLGPTVFANWG-D 121
TFGGQQKCGFSHNPAPAAIFRYEGAPDALPTDPGAAPKD------HQCLDTLDLS--PV 387
                                                                    LA-----KHTMTVIAAD----MVPVNAMTVDSLFMAVGQRYDVTIDASQAVGNYWFNI 336
                                                                                                                                                                              TLFSTNGEVSSFWGDVIQVNGQ-----PWPMLNVQP-RKYRFRFLNAAVSRSFALY 278
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Schneider, Palle
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                                                                                                                                                                                                                                                                                                                                                                                                                                         70; Mismatches 172;
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Pred. No. 1.
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US-09-028-887-2
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                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                      173 WYHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPL-VLTAKRY---NADG 228
                                                                                                                           122 TIEVTVNNHLRTNGTSIHWHGLHQKGTNYHDGANGVTECPIPPGGSRVYSFRARQYGTS- 180
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 24-Fe CLASSIFICATION:
                                                                                                                                                                                                     74 PNTG------VVRRYTFDI---TEVDNRPGPDGVIKEKLMLINDKLLGPTVFANWG-D 121
                                                                                                                                                                                                                                    69 PNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSP-------GPTIIVPRGTE 117
                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                   TLFSTNGEVSSFWGDVIQVNGQ-----
                                                                                                                                                                SVVRFVNSGENTSPNSVHLHGSFSRAP----FDGWAEDTTQPGEYKDYYYPNRQAARML 172
                                                  WYHSH-FSAQYGN----GVSGAIQINGPA----SLP----YDIDLGVLPLXDWYYKSADQ 227
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                                                                                                                                                                                                                                                                              137;
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24-February-1998
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25.2%;
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Pred. No. 1.7
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                 -PWPMLNVQP-RKYRFRFLNAAVSRSFALY 278
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                                                                                                                                                                                                                                                                                                             Length 616;
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RESULT 9
US-09-399-886-9
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; MOLECULE TYPE: US-09-399-886-9
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                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 50:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/9:
FILING DATE: December 18
FILING DATE: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61400920 No. 6140092disk of No. 6140092th America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cherry, Joel
TITLE OF INVENTION: LAC
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                                       TOPOLOGY:
                                                        STRANDEDNESS:
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Rasmussen, Grethe
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Svendsen, Allan
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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Best Local
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                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/396,260
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, Feng TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555
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                                                                                                                 COMPUTER:
                                                                                                                                                                   COUNTRY: USA
ZIP: 10174
                                                                                                                                                                                                 CITY: New York
STATE: NY
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CLASSIFICATION:
                                 FILING DATE:
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                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                 No. 6184015o No. 6184015disk of No. 6184015th America,
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25.2%;
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                                                                                                                                                                                                                                   Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -RDVTMLPARGWLLL-AFRTDNPGAWLFHCH
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                                                                                                                                    RESULT 11
US-09-518-901-2
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              Sequence 2, Application US/09518901
Patent No. 6218170
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                    NLIH
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                                                                                                                                                                                                                                                                                                                                                                  YVMNNDLSSIPVKNNIVRVDGVNEWTYWLVENDPEGRLSLPHPMHLHGHDFFVLGRSPDV 499
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                                                                                                                                                                                                                                                                                                                                                                                                  ---NRLLRNVP--RDTVEI------WRLENNSNG---WTHPVHIHLVDFRVLSRS--- 459
                                                                                                                                                                                                                                                                                                                                                                                                                                              VQKNVPVDGFVKEPGNTLPVTLHVDQAAAPHVFT-----WKING-SAADVDWDRPVLE 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLRDVP----FPEGGNWDPANPTDDE-----TFTFGRANGQWTINGVTFSDVE-----
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25.2%; Pred. No. 1.2
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Best Local Similarity
Matches 137; Conserv
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                                                                                                                                                                                                                                                                         337
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500 SPDSETRFVFDPAVDLPRLRGHNPVR----RDVTMLPARGWLLL-AFRTDNPGAWLFHCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 PNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSP------GPTIIVPRGTE 117
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/518,901
FILING DATE: 06-Mar-2000
CLASSIFICATION: <Unknown>
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NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
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APPLICATION NUMBER: 09/028,887
FILING DATE: <Unknown>
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ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                        NLRDVP----FPEGGNWDPANPTDDE-----TFTFGRANGQWTINGVTFSDVE-----
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                                                                                                                                                                              VQKNVPVDGFVKEPGNTLPVTLHVDQAAAPHVFT-----WKING-SAADVDWDRPVLE 439
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                                                                                                                                                                                                                                                                    TFGGQQKCGFSHNPAPAAIFRYEGAPDALPTDPGAAPKD-----HQCLDTLDLS--PV
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                                         -----TARGVEPYEAAGLKDVVWLARREVVYVEAHYAPFPGVYMLHCH 502
                                                                                        YVMNNDLSSIPVKNNIVRVDGVNEWTYWLVENDPEGRLSLPHPMHLHGHDFFVLGRSPDV
                                                                                                                                  ---NRLLRNVP--RDTVEI-----WRLENNSNG---WTHPVHIHLVDFRVLSRS---
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STATE: NY
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nilarity 25.2%;
Conservative 70
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Pred. No. 1.2e-15;
0; Mismatches 172;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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                                                                                                                            122 TIEVTVNNHLRTNGTSIHWHGLHQKGTNYHDGANGVTECPIPPGGSRVYSFRARQYGTS- 180
                                                                                                                                                                       118
228 LVIETLXKGNAPFSDNVLINGTAKHPTTGEGEYAIVKLTPDKRHRLRLINMSVENHFQVS 287
                               229 TLFSTNGEVSSFWGDVIQVNGQ-----PWPMLNVQP-RKYRFRFLNAAVSRSFALY 278
                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 50
                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
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                                                                                                                                                                                                     74 PNTG-----VVRRYTFDI---TEVDNRPGPDGVIKEKLMLINDKLLGPTVFANWG-D 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                               SVVRFVNSGENTSPNSVHLHGSFSRAP-----FDGWAEDTTQPGEYKDYYYPNRQAARML 17,2
                                                                 WYHSH-FSAQYGN---GVSGAIQINGPA----SLP-----YDIDLGVLPLXDWYYKSADQ 227
                                                                                                 WYHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPL-VLTAKRY---NADG 228
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Schneider, Palle
Rasmussen, Grethe
                                                                                                                                                                                                                                                                          Conservative
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25.2%;
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Pred. No. 1.2e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                   TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                              FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
MOLECULE TYPE:
                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 TFAGQS-----IDIRNLPGA-DGLGVEPEFDNTDKVMRFVVDEVLESPDTSEVPA 374
             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/4 FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                 LENGTH:
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                                                 620 amino acids
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AASLYNG, DOTTIT A.
ZENTION: PURIFIED MYCELIOPHTHORA LACCASES AND NUCLEIC
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                                                                                                                         212-867-0123
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Best Local Similarity
Matches 153; Conserv
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                   APPLICANT: Sorensen, Niels H.
TITLE OF INVENTION: Laccases with Improved Dyeing
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSE: No. 5948121disk of No.
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                                                                                                                                                                                  CITY: New York
STATE: NY
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APPLICATION NUMBER:
                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRNVP------RDTVEIWRLENNSNG---WTHPVHIHLVDFRVLSRSTARG-- 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAKRYNA---DGTLFS-----TNGEVSSFWGDVIQVNGQPWPMLNVQPRKYRFRFLNAA 270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAAFNVTVLGDYGYNYTEFIDPMEPLWRPRPFLLGEFENGSGDFSELAITDRIQEMASFN 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQNTSFPPGYNIVEVNGADQWSYWLIENDPGAPFTLPHPMHLHGHDFYVLGRSPDESPAS 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTS-WYHSH-FSAQYGN---GVVGAIQINGPA--SLPYDTDLGVFPISDYYYSSADELVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDTIQVTVINNLE-TNGTSIHWHGLHQKGTNLHDGANGITECPIPPKGGRKVYRFKAQQY 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VEPYEAAGLKDVVWLARREVV-----YVEAHYAPFPGVYMLHCHNLIHEDHDM 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTSEVPANLRDVPFPEGGNWDPANPTDDETFTFGRANGQWTINGVTFS-----DVENRL 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TFAGQSI------DIRNLPGADGLGVEPEFDNTDKVMRFVVDEVLESP 367
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                                                                                                                                                                                                                       405 Lexington Avenue
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US/09/083,485
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APPLICANT:

BERKA,

Randy Michael

Sequence 2, Application US/08939218A Patent No. 5981243 GENERAL INFORMATION:

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RESULT 15
US-08-939-218A-2
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION:
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                                                                       PYPKSD
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                                                                                                                                                                  MAAFNVTVLGDYGYNYTEFIDPMEPLWRPRPFLLGEFENGSGDFSELAITDRIQEMASFN 571
                                                                                                                                                                                                      NERHVFDPARDAGLLSGANPVRRDVTMLPAFGWVVLAFRADNPGAWLFHCHIAWH-----
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Pred. No. 1.4e-15;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BROWN, St.
APPLICANT: XU, Feng
APPLICANT: SCHHEIDER
APPLICANT: OXENB LL,
APPLICANT: OXENB LL,
APPLICANT: OXENB LL,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, CATOL E.
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
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                                     384 NIKPVVA--RDVPL-SGFAKRPDNTLDVTLDTTGTPLFVWKVNGSAINIDWGRPVVDYVL 440
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STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
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TELEFAX: 212-878-9655
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                 DTSEVPANLRDVPFPEGGNWDPANPTDDETFTFGRANGQWTINGVTFS-----DVENRL 421
                                                                                                                                                                                                                                VSRSFALYLATSEDSETRLPFQVIAADGGLLEGPVD---TDTLYISMAERWEVVIDFS-- 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTESVVRFVNSGENTSPNSVHLHGSFSRAP--FDGWAEDTTQP----GEYKDYYYPNRQA 168
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                                                                                                                                                       -----TFAGQSI------DIRNLPGADGLGVEPEFDNTDKVMRFVVDEVLESP 367
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AASLYNG, DOITIT A.
VENTION: PURIFIED MYCELIOPHTHORA LACCASES AND NUCLEIC VENTION: ACIDS ENCFODING SAME
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25.2%;
-RDTVEIWRLENNSNG---WTHPVHIHLVDFRVLSRSTARG--- 463
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Pred. No. 1.4e-
56; Mismatches
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1.4e-15;
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PYPKSD
                                                                                        MAAFNVTVLGDYGYNYTEFIDPMEPLWRPRPFLLGEFENGSGDFSELAITDRIQEMASFN 571
                                                                                                                                                    ----YEPYEAAGLKDVVWLARREVV----YVEAHYAPFPGVYMLHCHNLIHEDHDM
                                                           ---VSGGLGVVYLERADD---
603
                                                          LRGAVSDADADDLDRLCADWRRYWPT-N 597
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Search completed: October 3, 2002, 10:54:52 Job time: 36 sec

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Com
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/SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1983.DAT:*
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/SIDS1/gcgdata/hold·geneseq/geneseqp-emb1/AA1986.DAT:*
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                 AAB81505
AAB20097
AAB810097
AAB840843
AAY69204
AAY95538
AAY95538
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AAY96763
AAY96763
     AAY399,92
                                                                                                                                                                                                               SUMMARIES
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1101.668 Million cell updates/sec
Amino acid sequenc
Bipolarius spicife
Bipolaris spicifer
Curvularia pallesc
Curvularia pallesc
Stachybotrys chart
Stachybotrys pheno
                                                                                                Stachybotrys chart
Stachybotrys chart
Bilirubin oxidase.
Bilirubin oxidase.
                                                                                                                                                                    Description
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Myceliophthora the	AAW79078	19	573	7.2	225	45
Myceliophthora the	AAW76317	19	573	7.2	225	44
Myceliophthora the	AAW79077	19	573	7.3	26	43
	AAW76316	19	573	7.3	226.5	42
M. thermophila lac	AAY50729	21	620	7.7	241	41
	AAW16302	18	620	7.7	241	40
	AAR88500	17	620	7.7	241	39
Myceliophthora the	AAY91085	21	573	7.7	241	38
	AAW63124	19	573	7.7	241	37
	AAW51782	19	573	7.7	241	36
	AAW62503	19	573	7.7	241	35
	AAW59913	19	573	7.7	241	34
	AAW76315	19	573	7.7	241	ω
	AAW79079	19	573	7.8	243	32
0	AAW19855	18	620	8.1	253	31
	AAY91086	21	616	8.1	53	30
-	AAW51783	19	616	8.1	5	29
	AAW62502	19	616	8.1	253.5	28
	AAW59915	19	616	8.1	53	27
	AAW76314	19	616	8.1	5	26
ytalidium th	AAW18060	18	616		54	25
S. epidermidis ope	AAG82886	22	348	10.1	313	24
Amerosporium atrum	AAY96764	21	113	11.0	342	23
	AAY95540	21	113	11.0	342	22
. epidermidis	AAG83082	22	410	11.4	355.5	21
a	AAG83078	22	477	4.	453	20
	AAG44480	21	581	14.6	454	19
Arabidopsis thalia	AAG44481	21	574	14.6	454	18
Arabidopsis thalia	AAG44482	21	570	4	454	17
Corynebacterium gl	AAB79105	22	497	6	498.5	16
C glutamicum prote	AAG90799	22	511	6	504	15
н	AAU04831	22	474	19.4	605	14
	967	21	594	55.1	1716.5	
Stachybotrys chart	AAY95537	21	594	55.1	1716.5	12

ALIGNMENTS

AAB81505 RESULT

Н

AAB81505 standard;

Protein;

583

A

AAB81505;

18-JUN-2001

(first entry)

Stachybotrys chartarum phenol oxidase B enzyme

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New detergent compositions comprising a phenol oxidizing enzyme useful
                  WPI; 2001-273462/28.
N-PSDB; AAF82586.
                                                                                                                                                                                      Stachybotrys phenol oxidase B; spoB; phenol oxidising enzyme; detergent; paper production; pulp production; textile; food industry; bleaching.
                                            Convents D,
                                                            (UNIL ) UNILEVER NV.
(UNIL ) UNILEVER PLC.
(HIND-) HINDUSTAN LEVER LTD.
                                                                                                                  06-SEP-2000; 2000WO-EP08840.
                                                                                                                                                     WO200121748-A1.
                                                                                                                                                                     Stachybotrys chartarum
                                                                                                22-SEP-1999; 99EP-0203120
                                                                                                                                     29-MAR-2001.
                                            Doornink M,
                                            De
                                            Vries
                                            CH,
                                           Wang
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10.35

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AAB20097
ID AAB2
XX
AC AAB2
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DT 23-A
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a Stachybotrys chartarum phenol oxidising enzyme. The invention relates to detergent compositions comprising one compression and a phenol oxidising enzyme having at least 68% identity to the Stachybotrys chartarum phenol oxidising enzyme. Phenol oxidising enzymes may be used in the detergent, paper, pulp, textile and food industries. They are used for preventing the transfer of dyes in solution from one textile another during detergent washing, or in modifying the colour associated with dyes and coloured compounds having different chemical structures, such as in pulp and paper bleaching, bleaching the colour of stains on fabric and in detergent and textile
 23-APR-2001
                        AAB20097;
                                                AAB20097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                       RPFLLGEFENGSGDFSELAITDRIQEMASFNPYAQADDDAAEE 583
                                                                                                                                                                                                    REVVYVEAHYAPFPGVYMLHCHNLIHEDHDMMAAFNVTVLGDYGYNYTEFIDPMEPLWRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAPNTYPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMYGYDGMSPGPTIIYPRGTESVV 120
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                                                                                                                                                       revvyveahyapfpgvymlhchnlihedhdmmaafnvtvlgdygynytefidpmeplwrp
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                                               standard;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                AAF30028). The invention provides phenol oxidising enzymes such as phenol oxidase B, or enzymes having at least 68% identity to it, nucleic acids encoding them, expression vectors, filamentous fungus and yeast host cells, and methods for the recombinant production of the phenol oxidising enzymes. The enzymes are useful for bleaching pulp and paper, fabric stains, and in detergent and textile applications. They show optimal activity at pH range 5-11, 7-10.5 or 8-10, and at 20-60 or 20-40 degree C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New phenol oxidizing enzyme, also useful in the detergent, paper pulp, textile or food industries, especially in modifying the colassociated with dyes and coloured compounds, as well as in anti-cassociated with dyes and coloured compounds.
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              phenol oxid
AAF30028).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transfer
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DB; AAF30028, AAF20029.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        oxidase
                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             applications
                                                                                                                                                                                                                                                                                                                                              583
                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence is that of Stachybotrys chartarum ase B, as deduced from isolated genomic DNA
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; 23pp; English.
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tile; detergent.
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Matches 578
                                                                                                                   The present sequence was used for comparison with the Stachybotrys chartarum phenol oxidising enzyme. The invention relates to detergent compositions comprising one or more surfactants and a phenol oxidising enzyme having at least 68% identity to the Stachybotrys chartarum phenol oxidising enzyme nazyme. Phenol oxidising enzymes may be used in the detergent paper, pulp, textile and food industries. They are used for preventing the transfer of dyes in solution from one textile to another during;
                                                                             detergent washing, or in modifying the colour associated with dyes and coloured compounds having different chemical structures, such as in pul and paper bleaching, bleaching, the colour of stains on fabric and in detergent and textile applications.
                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                (UNIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bilirubin oxidase; phenol oxidising enzyme; phenol oxidase B; detergent; paper production; pulp production; textile; food i
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                                                                                                                                                                                                             Example 4; Fig 4; 46pp; English
                                                                                                                                                                                                                                   processing applications
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   Local Similarity
nes 578; Conser
                                                                                                                                                                                                                                          w detergent compositions comprising a phenol oxidizing enzyme useful detergent or cleaning compositions, fiber treatment, processing, nishing or production, paper and pulp production, or in starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w
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UNILEVER PLC
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           99.2%; Score 3090; 100.0%; Pred. No. 1
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  Mismatches
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           DB 22;
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                     Length
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         (AMAN ) AMANO
                          24-JAN-1992;
                                                                             JP05199882-A.
                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                                              RPFLLGEFENGSGDFSELAITDRIQEMASFNPYAQADD 578
                                                                                                                                                                                                                                                                                                                                       REVVYVEAHYAPFPGVYMLHCHNLIHEDHDMMAAFNVTVLGDYGYNYTEFIDPMEPLWRP
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                                                                                                       /label= sig_peptide 39..534
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Best Local Similarity
Matches 383; Conser
  fabric; p
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Phenol oxidizing enzyme; fungus; redox reaction; detergent; bleaching; fabric; pulp; paper; decolourisation; plant-derived food product; coloured compound; porphyrin; tannin; polyphenol; carotenoid;
                                                                                                        AAY69204 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-284681/36.
N-PSDB; AAQ47790.
                                          Amino acid sequence
                                                               30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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                                                                                                                                                         KDVVWLARREVVYVEAHYAPFPGVYMLHCHNLIHEDHDMMAAFNVTVLGDYGYNYTEFID
                                                                                                                                                                                                                                                      DVENRLLRNVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSRST---ARGVEPYEAAGL
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                                                                                                                                                                                                                                                                                                GLLEGPVDTDTLYISMAERWEVVIDFSTFAGQSIDIRNLPGA-DGLGVEPEFDNTDKVMR 357
                                                                                                                                                                                                                                                                                                                                                                    SFWGDVÍQVNGOPWHYNVOPRKYRFRELNAAVSRSFALYLATSEDSETRLPEQVIAADG 298
                                                                                                                                                                                                                                                                                                                                                                                                      mhitaenayrgqaglymltdpaedalnlpsgygefdipmiltskgytangnlvttngeln
                                                                                                                                                                                                  kdvvwlgrretvvveahyapfpgvymfhchnlihedhdmmaafnatvlpdygynatvfvd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISQAIGAVALGLAVIGGSSVDARSVAGRSTDMPSG-LTKRQTQLSPPLALYEVPLPIPP 59
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                                          of a phenol
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ed. No. 3.7e-174;
Mismatches 110;
                                        oxidising enzyme
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Best Local S
Matches 352
                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a phenol oxidizing enzyme from the fungus Acremonium murorum. The enzyme has the CBS accession number 157.72. The enzyme catalyses redox reactions and is specific for molecular oxygen as the electron acceptor. The phenol oxidising enzy is specifically used in detergents for bleaching entrains on fabrics, but also for bleaching pulp and paper and for decolourisation of plant-derived food products. The enzyme has a pH optimum in the plant-derived food products. The enzyme has a pH optimum in the almopunds, e.g. porphyrins, tannins, polyphenols, carotenoids, anthocyanins and Maillard reaction products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phenol-oxidizing enzyme from Acremonium, for bleaching stains on fabrics -
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                                            AIGAVALGLAVIGGSSV------DARSVAGRSTD------MPSGLTKRQTQLS
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DB; AAZ61243.
           VEPEFDNTDKVMRF-VVDEVLESPDTSEVPANLRDVPFPEGGNWDPANPTDDETFTFGRA
                                                                  SETRLPFQVIAADGGLLEGPVDTDTLYISMAERWEVVIDFSTFAGQSIDIRNLPGADGLG
                                                                                                                NADGTLFSTNGEVSSFWGDVIQVNGQPWPMLNVQPRKYRFRFLNAAVSRSFALYLATSED
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                                                                                                                                                                                                                                                     PPLALYEVPLPIPPLKAP-NTVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGM 104
ievnyddtdkvmrfnvaegplsspdtsvvpstlrdvpfpss----tsttidhsfrfart
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UNILEVER PLC.
HINDUSTAN LEVER
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 41-43;
                                                                                                                                                                                                                                                                                                                                                                                602
                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 1.3e
83; Mismatches
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L.3e-157;
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     Query Match
Best Local Sim
Matches 329;
                                                                                                                                                                                                                                                                                                                       phenol oxidising enzyme. The invention relates to detergent compositions comprising novel phenol oxidising enzymes that have at least 60% identity with the phenol oxidising enzyme of Stachybotrys chartarum (see ANY9537), and which are obtained from a bacterium, yeast or non-Stachybotrys fungus, especially B. spicifera, Curvularia pallescens (see ANY95539) and Amerosporium atrum (see ANY95540). The phenol oxidising enzyme is capable of modifying the colour associated with dyes or coloured compounds, and can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile
                                                                                                                                                                                                               fabric and for anti-dye transfer in detergent and textile applications. It may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidising enzyme, methods for producing the phenol oxidising enzyme, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bipolarius spicifera phenol oxidising enzyme.
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23-JUN-1999;
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                    New phenol oxidizing enzyme for modifying colors associated with or colored compounds, is obtained from fungus and is encoded by a nucleic acid comprising a specific nucleotide sequence
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Best Local
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ë
                                                                                                                                              Curvularia
                                                                                                                                                                                                                                      AAY95539 standard; Protein;
                          06-JUL-2000
                                                                                 Curvularia pallescens
                                                                                                                                                                            10-OCT-2000
                                                                                                             Phenol oxidising enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                      WO200039306-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347
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                                                                                                                                                                                                                                                                                                                           YGYN-YTEFIDPMEPLWRPRPFLLGEFENGSGDFSELAITDRIQEMASFNPYAQ 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QWTINGVTFSDVENRLLRNVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSR---STAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGTLFSTNGEVSSFWGDVIQVNGQPWPMLNVQPRKYRFRFLNAAVSRSFALYLATSEDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gptiivprgteavvrfinggdres--sihlhgspsrapfdgwaddmimkgeykdyyypnn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLALYEVPLPIPPLKAPNTVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSP 106
                                                                                                                                                                                                                                                                                                                                                                                       GVEPYEAAGLKDVVWLARREVVYVEAHYAPFPGVYMLHCHNLIHEDHDMMAAFNVTVLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ddyantdkvmrfhvss-qtvvdnsvvpeqlsqiqf----padktdidhhfrfhrtng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \tt qaarflwyhdhamhvtaenayfgqagaylitdpaedalglpsgygkydiplvlsskyyna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QAARMLWYHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPLVLTAKRYNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPTIIVPRGTESVVRFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYYYPNR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fgy nett dfhd ped prws arpft agdl tars gifsees ir arvnel aleq pyse\\
                                                                                                                                                                                                                                                                                                                                                                         gvmpyeaaglkdvvwlgrhetvlveahyapwdgvymfhchnlihedqdmmaafdvtklqn
                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt ewringigfadvenrvlakvprgtvelwelenssggwshpihvhlvdfrvvarygdegtr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRLPFQVIAADGGLLEGPVDTDTLYISMAERWEVVIDFSTFAGQSIDIRNLPGADGLGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dgtlktsvgedksvwgdiihvngqpwpflnveprkyrlrflnaavsrnfalyfvkqdnta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
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                                                                                                                                             pallescens phenol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  627 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.6%; Score 1762; DB 21; 61.6%; Pred. No. 1.7e-151; tive 71; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                 detergent; bleaching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
                                                                                                                                             oxidising
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                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of the Curvularia pallescens phenol oxidising enzyme. The invention relates to detergent compositions comprising novel phenol oxidising enzymes that have at least 60% identity with the phenol oxidising enzyme of Stachybotrys chartarum (see AAY95537), and which are obtained from a bacterium, yeast or non-Stachybotrys fungus, especially C. pallescens.

Elipolarius spicifera (see AAY95538) and Amerosporium atrum (see AAY95540). The phenol oxidising enzyme is capable of modifying the colour associated with dyes or coloured compounds, and can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. It may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidising enzyme, and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 322; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Fig 10; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIL ) UNILEVER NV.
(UNIL ) UNILEVER PLC.
(HIND-) HINDUSTAN LEVER LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methods for constructing expression hosts are provided
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23-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                        50 LYEVPLPIPPLKAPNTVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSPGPT 109
DNTDKVMRFVVDEVLESPDTSEVPANLRDVPFPEGGNWDPANPTD-DETFTFGRANGQWT
                                                                                                                       2000-514528/46.
                                                             antdkvmrfhvss-qavvdnsvvpaqlsqiqf-----padktgidhhfrfhrtnsewr
                                                                                                                                                       PFQVIAADGGLLEGPVDTDTLYISMAERWEVVIDFSTFAGQSIDIRNLPGADGLGVEPEF
                                                                                                                                                                                     lqtsvgednslwgdvihvngqpwpffnveprkyrlrflnaavsrnfalyfvkqqatatrl
                                                                                                                                                                                                                                                                                                            iivprgteavvrfvnqgdres--sihlhgspsrapfdgwaedlimkgqfkdyyypnnqaa
                                                                                                                                                                                                                                                                                                                                         IIVPRGTESVVRFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYYYPNRQAA 169
                                                                                                                                                                                                                                                                                                                                                                        lfrealpippakepnkmtnpvtnkeiwyyeivikpfnqqvypslrparlvgydgispgpt 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  627 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Der Velden S,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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99US-0338723.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   55.3%; Score 1723.5; DB 21; 60.6%; Pred. No. 5.6e-148; Live 72; Mismatches 122; I
                                                                                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Vries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627;
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                                                                                                                                                   Query Match
Best Local :
                                                                                                                                        Matches
                                                                                                                                                                                                                       This sequence is the Curvularia pallescens phenol oxidizing enzyme. Phenol oxidizing enzymes encoded by nucleic acid sequences which hybridize to the Stachybotrys chartarum DNA (AAA51313) are claimed, as long as the enzyme is capable of modifying the colour associated with dyes or coloured compounds. The enzymes are useful in detergent compositions and for modifying colors associated with dyes or coloured compounds which occur in stains in a sample. The enzymes are also useful for pulp and paper bleaching, anti-dye transfer in detergent and other textile applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1998;
23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Curvularia pallescens
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                               LYEVPLPIPPLKAPNTVPNPNTGEDILYYEMEIRPESHQIYPDLEPANNVGYDGMSPGPT 109
                                   ivprgteavvrfvnggdres--sihlhgspsrapfdgwaedlimkgqfkdyyypnnqaa 186
                                                 IIVPRGTESVVRFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYYYPNRQAA 169 (
                                                                                 {\tt lfrealpippakepnkmtnpvtnkeiwyyeivikpfnqqvypslrparlvgydgispgpt.} 128
                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-452191/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-YTEFIDPMEPLWRPRPFLLGEFENGSGDFSELAITDRIQEMASFNPYAQ 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYEAAGLKDVVWLARREVVYVEAHYAPFPGVYMLHCHNLIHEDHDMMAAFNVTVLGDYGY
              RMLWYHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPLVLTAKRYNADGT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nettdfhdpedsrwsarpftaadltarsgifseasirarvnelaleqpyse 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      paper
                                                                                                                                                                                                                                                                                                                                                  8; Fig 10; 45pp; English.
Similarity
                                                                                                                                                                                                                                                                                                                                                                            red compounds, acid comprisi
                                                                                                                                                                                                                                                                                                                                                                                                                             AAA51316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bodie EA;
                                                                                                                                                                                                                                                                                                                                                                         oxidizing enzyme for modifying colors associated with compounds, is obtained from fungus and is encoded by a id comprising a specific nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pallescens phenol
                                                                                                                                                                                                   627
                                                                                                                                      Conservative
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99US-0338723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme;
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                                                                                                                                                  55.3%;
60.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colour; dye; modification; detergent; stain;
                                                                                                                                  72;
                                                                                                                                     Score 1723.5;
Pred. No. 5.6e-
72; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oxidizing enzyme
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                                                                                                                                     .6e-148;
les 122;
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                                                                                                                                                           3 21;
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nettdfhdpedsrwsarpftaadltarsgifseasirarvnelalegpyse 589
                                                             PYEAAGLKDVVWLARREVVYVEAHYAPFPGVYMLHCHNLIHEDHDMMAAFNVTVLGDYGY
                                                                                                                                                                                              N-YTEFIDPMEPLWRPRPFLLGEFENGSGDFSELAITDRIQEMASFNPYAQ 575
                                                pyesaglkdvvwlgrhetvlveahyapwdgvymfhchnlihedqdmmaafdvtklqnfgy
                                                                                                                       INGVTFSDVENRLLRNVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSR----STARGVE
                                                                                                                                                antdkvmrfhvss-qavvdnsvvpaqlsqiqf----padktgidhhfrfhrtnsewr
                                                                                                                                                                        DNTDKVMRFVVDEVLESPDTSEVPANLRDVPFPEGGNWDPANPTD-DETFTFGRANGQWT
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RESULT 1 AAY45222 AAY45222 standard; Protein; 594 AA

detergent; Stachybotrys Stachybotrys 05-JAN-2000 AAY45222; anti-dye chartarum; phenol oxidising enzyme; colour; dye; chartarum phenol oxidising enzyme (first entry) transfer; stain removal; bleaching

30-SEP-1999. Stachybotrys 23-MAR-1999; WO9949010-A2 chartarum. 99WO-EP02042

(UNIL) UNILEVER NV. UNILEVER PLC

24-MAR-1998; 22-DEC-1998;

98US-0046969 98US-0218702

Wang Convents Ç Ď, Amory A, Wang Η, Dhaese P, Lambrechts-Rongvaux

A

N-PSDB; WPI; 1999-601211/51 AAZ25727

Detergent composition containing to bleach stains and prevent dye phenol or transfer oxidase from Stachybotrys, used

Claim 16; Fig 5; 56pp; English.

The present invention describes a detergent composition containing purified bhenol oxidising enzyme derived from Stachybotrys. The presequence represents Stachybotrys chartarum phenol oxidising enzyme enzyme can be used to modify the colour of dyes and other coloured compounds (e.g. for use in pulp and paper bleaching also for removistains, e.g. food, tea, blood etc., from fabrics) and for preventir transfer fabric washing The present enzyme. The removing Ø

QΥ

45

Matches 330; Query Match Best Local

Similarity

55.1%;

Score 1716.5; Pred. No. 2.26

2e-147; DB 20;

Conservative

67; Mismatches 125;

Indels

Gaps

Length 594; 19;

SO

Sequence

594

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RESULT 11
AAY39992
ID AAY399
XX
AC AAY399
XX
DE Stachy
XX
Phenol
KW Phenol
KW Fabric
XX
Stachy
XX
OS Stachy
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OS Stachy
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PR 23-MAF
PR 22-MAF
PR 22-MAF
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                      24-MAR-1998;
22-DEC-1998;
22-MAR-1999;
                                                                                                   WO9949020-A2
                                                                                                                     Stachybotrys
                                                                                                                                        Phenol oxidase; fabric washing;
                                                                                                                                                                    Stachybotrys phenol
                                                                                                                                                                                                            AAY39992;
                                                                                                                                                                                                                               AAY39992 standard; Protein;
                                                             23-MAR-1999;
                                                                                30-SEP-1999
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                                                                                                                                                                                                                                                                                                   578
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                                                                                                                      chartarum
                                                                                                                                                                                        (first
                     98US-0046969.
98US-0218702.
99US-0273957.
                                                             99WO-US06327
                                                                                                                                        enzyme; coloured compound; dye transfer prevention;
stain bleaching; anti-dye transfer; detergent.
                                                                                                                                                                    oxidase protein sequence.
                                                                                                                                                                                        entry)
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RESULT 12
AAY95537
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AC AAY955
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AC AAY955
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DT 10-OCT

AAY95537

standard;

Protein;

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AAY95537;

10-OCT-2000

(first

entry)

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel enzyme for modifying coloured dye-transfer - \ensuremath{^{\circ}}
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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DB; AAZ27601, A/
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                                                                         YPNRQAARMLWYHDHAMSITAENAYMGQAGVYMTODPAEDALNLPSGYGEFDIPLVLTAK
                                                                                                                                                                                                                                                                                                                          GMSPGPTIIVPRGTESVVRFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYY 162
                                                                                                                                                                                             sspnvripfqviasdagllqapvqtsnlylavaeryeilidftnfagqtldlrnvaetnd
                                                                                                                                                                                                                                                                                                               gmspgptfnvprgtetvvrfinna--tvensvhlhgspsrapfdgwaedvtfpgeykdyy 174
                                    {\tt tameekgylqedfedpmnpkwravpynrndfharagnfsaesitarvqelaeqepynrld}
                                                                                                                                                                           LGVEPEFDNTDKVMRFVVDE-VLESPDTSEVPANLRDVPFP---EGGNWDPANPTDDETF
                                                                                                                                                                                                                EDSETRLPFQVIAADGGLLEGPVDTDTLYISMAERWEVVIDFSTFAGQSIDIRNLPGADG
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Query Match
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Matches 330; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of a phenol oxidising enzyme Stachybotrys chartarum MUCL 38898. A claimed detergent co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 5A-B; 45pp; English.
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23-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p and paper bleaching, for bleaching the colour of stains on ric and for anti-dye transfer in detergent and textile lications. It may also be capable of modifying the colour in absence or presence of an enhancer. Expression vectors and t cells comprising a nucleic acid encoding a phenol oxidising
                                                                                                                                                                                                                                                YPNRQAARMLWYHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPLVLTAK 222
                                                                                                                                                                                                                                                                                                                                                          GMSPGPTIIVPRGTESVVRFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYY 1620
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sspnvripfqviasdagllqapvqtsnlylavaeryeiiidftnfagqtldlrnvaetnd
                                                                                                                                   RYNADGTLESTNGEVSSEWGDVIQVNGQPWPMLNVQPRKYRFRELNAAVSRSFALYLATS, 282
                                                                                                                                                                                                         fpnyqsarllwyhdhafmktaenayfgqagayiindeaedalglpsgygefdipliltak 234
                                                                                                                                                                                                                                                                                                                         gmspgptfnvprgtetvvrfinna--tvensvhlhgspsrapfdgwaedvtfpgeykdyy 174
                                                                                                       yynadgtlrstegedqdlwgdvihvngqpwpflnvqprkyrfrflnaavsrawllylvrt. 294
                                                                                                                                                                                                                                                                                                                                                                                                                                sppynllyrnalpippvkqpkmiitnpvtgkdiwyyeieikpfqqriyptlrpatlvgy
                                                     EDSETRLPFQVIAADGGLLEGPVDTDTLYISMAERWEVVIDFSTFAGQSIDIRNLPGADG
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99US-0338723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1716.5; DB 21; Length 594; Pred. No. 2.2e-147; 77; Mismatches 125; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De
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Query Match Best Local Similarity

55.1%; 61.0%;

Score 1716.5; DB 21; Pred. No. 2.2e-147;

Length 594;

Sequence

594

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                                                       hybridize to the coding DNA are claimed, as long as the enzyme is capped of modifying the colour associated with dyes or coloured compounds. The enzymes are useful in detergent compositions and for modifying colors associated with dyes or colored compounds which occur in stains in a
                           sample. The enzymes are also useful for pulp and paper bleaching, anti-dye transfer in detergent and other textile applications.
                                                                                                                                                                                                  or colored compounds, nucleic acid comprisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phenol oxidizing enzyme; pulp; paper bleaching.
                                                                                                                                                                  Claim 1; Fig 5A-B; 45pp; English
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                                                                                                                                                                                                                             New phenol oxidizing enzyme for modifying colors associated with dyes
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                                                                                                                                                                                                                                                                                                                                          (GEMV ) GENENCOR INT
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23-JUN-1999;
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DB; AAA51313, AAA51314.
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                                                                                                                   s the sequence of Stachybotrys chartarum phenol oxidizing oxidizing enzymes encoded by nucleic acid sequences which
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N-PSDB; AAS08693
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                                                                                                                                                               Micromonospora
                                                                                                                                                                                               Everninomicin; fermentation; 7
                                                                                                                                                                                                                               Micromonospora
                                                                                                                                                                                                                                                                                                AAU04831 standard; Protein; 474
                              Hosted TJ,
                                                    (SCHE ) SCHERING CORP
                                                                           12-JAN-2000;
                                                                                                12-JAN-2001; 2001WO-US01187
                                                                                                                    19-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMSPGPTIIVPRGTESVVRFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sppynllyrnalpippvkqpkmiitnpvtgkdiwyyeieikpfqqriyptlrpatlvgyd 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPPL-ALYEVPLPIPPLKAPN-TVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYD 102
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                               Horan AC,
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                                                                           2000US-0175751
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                              antibiotic; bottle-neck gene; orthomicin; Tailoring gene product; oxidase;
                                                                                                                                                               carbonacea var. africana
                                                                                                                                                                                                                               everninomicin biosynthetic enzyme evrG
                              Wang
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The sequence represents a Tailoring gene product, an oxidase, CC everg. The protein comprises one of 98 enzymes of the CC everninomicin antibiotic biosynthetic pathway. A vector comprising a CC M. carbonacca everninomicin biosynthetic pathway resistance gene product is useful for selecting for a transfected or transformed host cell. An cintegrative version of the vector is useful for introducing a cyarninomicin pathway gene (a bottle-neck gene) into an actinomycete of the genus Micromonospora. The DNA encoding the biosynthetic proteins is cuseful for synthesising novel everninomicin-related compounds, arising cfrom modifications of the DNA sequence designed to change glycosyl and condified orsellinic acid groups contained in everninomicin, for expressing functional or mutant everninomicin biosynthetic enzyme for evaluation, diagnosis and preferably biosynthesis of everninomicin or cother secondary metabolic products, improving the yield of everninomicins of the produce novel everninomicins and also as a hybridisation probe to identify homologous sequences. The encoded polypeptides are useful for combinatorial biosynthesis to generate libraries of orthomycins, e.g. ceverninomicin analogues/homologues and drug discovery. The DNA encoding the integrase allows for increasing a given gene dosage. The integrate genes which increase the yield of known products or to generate coverly such as hybrid antibiotics or other novel secondary metabolites or order to carry out bioconversions with compounds to which the strain is normally sensitive and is thus useful in fermentation or compounds to processes involving a given gene and to carry out bioconversions with compounds to which the strain is normally sensitive and is thus useful in fermentation or carries and integrate and is thus useful in fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid molecules encoding everninomicin pathway gene products, useful for improving yields of everninomicin, to proverninomicin and as probes to identify homologous sequences -
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Best Local Similarity
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                                                                                         GGNWDPANPTDDET----FTFGRANGOWTINGVTFSDVENRLLRNVPRDTVEIWRLENNS 439
                                                                                                                                                                                                                  FRFLNAAVSRSFALYLATSEDSETRLPFQVIAADGGLLEGPVDTDTLYISMAERWEVVID
                                                                                                                                                                                                                                                                                                         dghpmdlippggskvydypnlqrgatlwyhdhthayeadhvyrglhgfyliddpaehhlr 190
tdpfpfdhpfhlhlvtfrvlgrd--ggppapedaglkdtvyvspkgsvkiqvtfatpylg
                              NG----WTHPVHIHLVDFRVLSRSTARGVEPYEAAGLKDVVWLARREVVYVEAHYA-PFPG
                                                          g-----tptvertvsmsfdmsarppialmdgkpfdpl--rvdvqvkrgsteiwnvvnad
                                                                                                                                                     FSTFAGQSIDIRNLPGADGLGVEPEFDNTDKVMRFVVDEVLESPDTSEVPANLRDVPFPE
                                                                                                                                                                                                                                                              LPSGYGEFDIPLVLTAKRYNADGTLFSTNGEVSSFWGD--VIQVNGQPWPMLNVQPRKYR 263
                                                                                                                                                                                                                                                                                                                                                               HQIYPD-LEPANMVGYDGMSPGPTIIVPRGTESVVRFVNSGENTSPNSVHLHGSFSRAPF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGRSTDMPSGLTKRQTQLSPPLALYEVPLPIPPLKAPNTVPNPNTGEDILYYEMEIRPFS
                                                                                                                     faehagg----
                                                                                                                                                                                   frllnaalkhvfrlnlgge-----pltriatdggllpaptshtelalssgerveivid
                                                                                                                                                                                                                                              lpa--gkydvpimlrnaqfddsgal-----vfghpddrvtilangkaqpyfevaprryr
                                                                                                                                                                                                                                                                                                                                       DGWAEDTTQPGEYKDYYYPNRQAARMLWYHDHAMSITAENAYMGQAGVYMIQDPAEDALN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                aghaapvpsrvstttvavtp----ftepmpvpprltp---vsrrdgidv--yeipirpaq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.4%;
35.1%;
                                                                                                                       -gpvylydgdnpilrfdvssravt-dpsrvpvtlralp-pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 605; DB 22;
Pred. No. 3.2e-46;
8; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 474;
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RESULT 1

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AAG90799 standard;

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                                                                                                                                                                        Matches 157;
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Best Local
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of nucleotide and protein ... sequences from the Coryneform bacterium Corynebacterium glutamicum, These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described to the coryneits of the inventor of the protein described to the coryneits of the inventor of the present sequence is a protein described to the coryneits of the inventor of the protein described to the coryneits of the inventor of the present sequence is a protein described to the coryneits of the inventor of the protein described to the coryneits of the inventor of the coryneits of the inventor of the present sequence is a protein described to the coryneits of the inventor of the present sequence is a protein described to the coryneits of the inventor of the present sequence is a protein described to the coryneits of the inventor of the present sequence is a protein described to the coryneits of the inventor of the present sequence is a protein described to the coryneits of the coryneits 
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                                                                                                                                                                                                                                                                                                                                       in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KYOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17;
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                            Sequence
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                              61
                                                                         12
                                                                                                                                                                                               Local Similarity
KAPNTVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMYGYDGMSPGPTIIVPRGTESVY 120
                                                                                                         GAVALGLAVIGG-----SSVDARSVAGRSTDMPSGLTKRQTQLSPPLALYEVPLPIPPL 60
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                                                                      gagvlaatvvgaqvlvacssddvrgyggepr-----
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; 2000JP-0159162.
; 2000JP-0280988.
                                                                                                                                                                        Conservative
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da M, Ozaki A;
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                                                                                                                                                                      Score 504; DB Pred. No. 5.9e 72; Mismatches
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5.9e-37;
nes 232;
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                                                                                                                                                                                                                 Length 511;
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                     KDVVWL---ARREVVYVEAHYAPFPGVYMLHCHNLIHEDHDMMAAFNVTVLGD 522
                                                                                                    DVENRLLR---NVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSRSTARGVEPYEAAGL 472
                                                                                                                                                                     MRFVVDEVLESPDTSEVPANLRDVPFPEGGNWDPANPTDDETFTFGRANGQWTINGVTFS 415
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kdtvglppgatatlavefghypdpqwpymyhchmlyhedqgmmgqfvivepgd 489
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ALIGNMENTS

RESULT 1

B48521

bilirubin oxidase (EC 1.3.3.5) - fungus (Myrothecium verrucaria)

C;Species: Myrothecium verrucaria

C;Species: Myrothecium verrucaria

C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C;Accession: B48521; A48521

R;Koikeda, S.; Ando, K.; Kaji, H.; Inoue, T.; Murao, S.; Takeuchi, K.; Samejima,

J. Biol. Chem. 268, 18801-18809, 1993

A;Title: Molecular cloning of the gene for bilirubin oxidase from Myrothecium ver

A;Reference number: A48521; MUID:93366794

A;Accession: B48521. Qy A;Molecule type: mRNA; protein
A;Residues: 1-572 <KOIZ>
A;Cross-references: GB:D14081; NID:g436236; PIDN:BAA03166.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:136728, C;Keywords: oxidoreductase A;Molecule type: DNA A;Residues: 1-572 <KOII> A;Cross-references: GB:D14081; NID:g436236; PIDN:BAA03166.1; PID:g456710 A;Note: sequence extracted from NCBI backbone (NCBIN:136730, NCBIP:136732) QΥ Вþ QY рЬ Вb 20 Дb Qγ 멍 Ωy A; Accession: A48521 A; Status: preliminary A; Status: preliminary Matches Query Match
Best Local Similarity 236 176 179 MSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPLVLTAKRYNADGTLFSTNGEVS 118 299 GLLEGPVDTDTLYISMAERWEVVIDFSTFAGQSIDIRNLPGA-DGLGVEPEFDNTDKVMR 119 296 GLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNLGGSIGGIGTDTDYDNTDKVMR 58 1 MFKHTLGAAALSL-LFNSNAVQASPVP--ETSPATGHLFKRVAQISPQYPMFTVPLPIPP 1 MISQAIGAVALGLAVIGGSSVDARSVAGRSTDMPSG-LTKRQTQLSPPLALYEVPLPIPP VVRFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYYYPNRQAARMLWYHDHA.178 SFWGDVIHVNGQPWPFKNVEPRKYRFRFLDAAVSRSFGLYFADTDAIDTRLPFKVIASDS SFWGDVIQVNGQPWPMLNVQPRKYRFRFLNAAVSRSFALYLATSEDSETRLPFQVIAADG VVRFINNAE--APNSVHLHGSFSRAAFDGWAEDITEPGSFKDYYYPNROSARTLWYHDHA MHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSKQYTANGNLYTTNGELN VKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLGSADLVGYDGMSPGPTFQVPRGVET 383; Conservative 64.5%; 65.4%; 71; Score 2010; Pred. No. 1 Mismatches .1e-135; DB 2; 110; Length Indels PID:g456710 NCBIP:136729) 22; Myrothecium verruca Gaps 357 295 298 175 57 59 10;

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Spore coat protein (outer) cotA - Bacillus subtilis

C;Species: Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999.

C;Accession: F69604; A27393; S02538

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C; Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390; 249-256, 1997

A;Authors: Toulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-Positive bacterium Bacillus subtilis.

A;Accession: F69604
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A; Status: not compared v
A; Molecule type: DNA
A; Residues: 1-32 < SAN>
C; Comment: this spore co
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A;Gene: cotA
C;Keywords:
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A;Accession: A27393
A;Status: not compared with conceptual translation A;Molecule type: DNA
A;Residues: 1-37 < CDON>
R;Sandman, K.; Kroos, L.; Cutting, S.; Youngman, P.;
J. Mol. Biol. 200, 461-473, 1988
A;Title: Identification of the promoter for a spore caseference number: S02538; MUID:88286730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12449.1; A;Experimental source: strain 168
R;Donovan, W.; Zheng, L.; Sandman, K.; Losick, R.
J. Mol. Biol. 196, 1-10, 1987
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Residues: 1-513 <KUN>
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57 IPPLKAPNTVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSPGPTIIVPRGT 116
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A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: B86364
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F19G10.5 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
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B86364
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A; Residues: 1-568 <STO>
A; Cross-references: GB:
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                                                                                  IKPASLQIGMFSTKWKFHRDL-PATPVFAYGTSRSKATVPGPTIETVYGVDTYVTWRNHL 108
                                                                                                                              IRPFSHQI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASYPSVQHERIQNIRTLKLAGTQDE---YGRPVLLLNNKRW------HDPVTETP
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                                                                                                                                                                                            Similarity
                                                                                                                                                                        15.7%; Score 489.5; DB 2; ilarity 28.3%; Pred. No. 4.3e-27; Conservative 77; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                GB:AE005172; NID:g2462832; PIDN:AAB72167.1; GSPDB:GN00141
                                                                                                                              ---YPDLEPANMVGYDGMS-----PGPTIIVPRGTESVVRFVNSG 126
                                       -PNSVHLHGSFSRAPFDGWAE-----
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Alon

Kim,

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probable exported protein YPO3409 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AC0414
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; ideno-Tarraga, A.M.; Chillingworth, T.; Stepton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AL590842; PIDN:CAC92639.1; PID:g15981336; GSPDB:GN00175 C;Genetics: A;Gene: YPO3409
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A;Molecule type: DNA
A;Residues: 1-533 <KUR>
                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AC0414
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 DPAEDALNLPSGYGEFDIPLYLTAKRYNADGTLFSTNGEVS----
                                                                     GSFSRAPFDGWAEDTTQPGEYKDYYYPNRQAARMLWYHDHAMSITAENAYMGQAGVYMIQ 197
                                                                                                                  QIYPDLEPANMV------GYDGMSPGPTIIVPRGTESVVRFVNSGENTSPNSVHLH 13.
                                                                                                                                                          GLEIPGEVDGGPQALIQPGAKRQVTFAVEQPAATCWFHPHTHSKTGHQVAMGLGGLVLID
                                                                                                   KINLNIQTGSVVWLPSTATQTWGYNGNLLGPAIRLQRGKAVTIDITNALPEAT--TVHWH
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                                                                                                                                                                                                                                 14.8%;
                                                                                                                                                                                                                  ; Score 460; DB 2; I
; Pred. No. 5e-25;
62; Mismatches 210;
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666
A;Recession: C70397
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-527 <AQF>
A;Cross-references: GB:AE000724; NID:g2983585; PIDN:AAC07157.1; PID:g2983586; GB
A;Experimental source: strain VF5
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: C70397
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                                                                 SSGQLVYNPMGHM-GFWGDTILVNLTPNPYMDVERKIYRFRILNGSNARPYRLALLRGNQ
                                                                                                                            ADGTL-FSTNGEVSSFWGDVIQVNGQPWPMLNVQPRKYRFRFLNAAVSRSFALYLATSED
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spore coat protein-like protein, 24980-21957 [imported] - Arabidopsis thaliana C. Species: Arabidopsis thaliana (mouse-ear cress)  
C. Species: Arabidopsis thaliana (mouse-ear cress)  
C. Accession: G96734  
R. Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.; Recense number askeid41; MUID:21016719
A.; Status: preliminary
A.; Status: preliminary
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A;Residues: 1-591 <STO>
A;Cross-references: GB:Al
C;Genetics:
A;Gene: F23N20.3
A;Map position: 1
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                                                         ---LDFIVVGSDSAYLAKPVSTKSVLLAPSEIVDVLVDFSKSTSKTAILANNAPYPYPSG
                                                                                             ETRLPFQVIAADGGLLEGPVDTDTLYISMAERWEVVIDFSTFAGQSIDIRN---LPGADG
                                                                                                                                                          -STNGEVSSFW-----GDVIQVNGQPWPMLNVQPRKYRFRFLNAAVSRSFALYLATSEDS
                                                                                                                                                                                                                     DHAAGLTRVNLLAGLLGSYILRHSSVESPLRLPTG-REFDRPLVIFDRSFRKDGSIYMNA
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A; Residues: 1-494 <KUR>
A; Cross-references: GB:
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                                                                                                                                        --DVPFPEGGNWD--
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28.7%;
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756888
A;Accession: AC3582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable blue-copper protein yacK precursor [imported] - Brucella melitensis (strain C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 LVIASDGGFISQPVSIEQLTISPGERYEVLVDFSN--GEAVDLVTYGDNGSGDGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 RGTESVVRFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYKDYYYPNRQAARMLW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531 GWKNVFKMMPGHVTKILVRFSYIHSNESYSFDATQEPG-YVYHCHILDHEDNMMMRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 SG-ESVTLSVENAMD-EETTLHWHGLFVPSHLDGGPHNVIAPGAKWEPKVAVNQPASFNW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 PLPIPPLKAPNTVPNPNTGEDILYYEMEIRPFSHQIYPDLEPANMVGYDGMSPGPTIIVP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVIAADGGLLEGPVDTDTLYISMAERWEVVIDFSTFAGQSIDI---RNLPGADGLGVEPE 348
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                                                                                S----DVENRLLRNVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSRSTARGVEPYEAA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHPHLHGHTARQAHMGIAGLMIVRDGKDAERGLPETYGVDDLPLVLQDRRVIEGDAVYAP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPLVLTAKRYNADGTLFST
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                                                                                                                                                                     PSSNPHASGDDMDHMEMGSMAGMDHDMHGSRSAADAGPALD-ALTSG----VQMAIADKPF
                                                                                                                                                                                                                                                                                                                                                                                                                   FDNTDKVMREVVDEVLES----PDTSEVPA-----
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                                                                                                                                                                                                                                                                                                                                      ----HLMRFTVDPALEGRVAKPPVSLDGPÄAPDEKLSVQRRSFFFDERMAENMKLMMRQ
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-GSWEIWEL--TSREMAHPFHIHGASFRILSMNGKK--PPAHQT
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Pred. No. 5.6e-22;
                                                                                                                                                                                                                                                      -PANPTDDETFTFGRANGQWTINGVTF 414
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A; Molecule type: DNA
A; Residues: 1-516 <HAY>
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Best Local
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             Genome
                                          .; Grotbeck, E.J.
09, 529-533, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVTLNVDQPAATCWFHPHQHGKTGRQVAMGLAGLVVIEDDEILKLMLPKQWGIDDVPVIV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYDGMSPGPTIIVPRGTESVVRFVNSGENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEYK 159
                                                                                                                                                                                                                                                                                                                                                                                    PAAHRAGWKDTVKVEGNVSEVLVKFNHDAPKERAYMAHCHLLEHEDTGMMLGFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --KINGQAFD--MNKPMFAAAKGQYERWVISGVGDMMLHPFHIHGTQFRILSEN---GKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QWTINGVTFSDVENRLLRNVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSRSTARGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLSMDPMLDMMGMQMLMEKYGDQAMVGMDHSQMMGHMGHGNMNHMN--HGGKFDFHHAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLPVSQMGMAIAP-FDKPHPVMRIQPIAISASGALPDTLSSLPA----LPSLEGLTVRKL 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAKRYNADGTL - - - FSTNGEVSSFWGDVIQVNGQPWPMLNVQPRKY - RFRFLNAAVSRSF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYYYPNRQAARMLWYHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPLVL
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sequence of enterohemorrhagic Escherichia coli 0157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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29.7%;
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Pred. No. 9.9e-22;
6; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GNWDPANPTDDETFTFGRANG 405
                                                                                                                                                                                                                   Escherichia coli (strain 0157:H7, substrain
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                                                                                                  J.D. . Rose,
                                                                     Potamousis,
                                                                                                                                                          14-Sep-2001
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                                                                 D.J.;
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      A; Experimental source:
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strain

W3110

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probable copper-binding protein yack - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999 C;Accession: C64735; S45200 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; l.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: C; Genetics:
                                                                                                                                                                  A; Experimental source: strain R; Fujita, N.
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A;Cross-references: GB:AE005174; NID:g12512835; PIDN:AAG54427.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
                                  A; Molecule type: DNA
A; Residues: 1-463, 'LIARAG', 470, 'IPLR'
A; Cross-references: EMBL:D26562; NID:
                                                                                                                                                                                                                                                                                                    Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of it A:Reference number: A64720; MUID:97426617
A;Accession: C64735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
C64735
                                                                                                   A; Reference number: A; Accession: S45200
                                                                                                                           submitted to the EMBL Data Library, A; Reference number: S45181
                                                                                                                                                                                       A;Cross-references: GB:AE000121; GB:U00096; NID:g1786306; PIDN:AAC73234.1; PID:g17863A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-516 <BLAT>
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A; Residues: 1-516 <S
                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown;
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29.7%;
5562; NID:g473770;
n K-12, substr
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Pred. No. 9.9
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                                  PIDN:BAA05579.1;
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                                     PID:d1006123;
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                                  PID:9473
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C; Genetics: A; Gene: yack
C; Keywords: c
                                                                                                                                                                                                                                                                                                                                                                                                                                        probable multicopper oxidase precursor [imported] - Salmonella enterica subsp. C:Species: Salmonella enterica subsp. enterica serovar Typhi A:Note: this species has also been called Salmonella typhi C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C:Accession; AF0523 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
AF0523
                                                                                                                                                                                                                                                                                         A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J. A;Title: Complete genome sequence of a multiple drug resistant Salmonella A;Reference number: AB0502; PMID:11677608
A;Accession: AF0523
A;Status: preliminary
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                                                                                                                                                                                       A;Cross-references: GB:AL513382; PIDN:CAD01326.1; PID:g16501454; GSPDB:GN00176 C;Genetics: A;Gene: yacK
                                                                                                                                                                                                                                                                                                                                                                                                     , S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001
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A; Residues: 1-536 < PAR>
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Best Local Similarity
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                                       100 GYDGMSPGPTIIVPRGTESVVRFVNS-GENTSPNSVHLHGSFSRAPFDGWAEDTTQPGEY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
68 GYNGNLLGPAVQLHKGKSVTVDIHNQLAEDT---TLHWHGLEIPGIVDGGPQGIIPAGGT 124
                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-YEAAGLKDVVWLARR--EVVYVEAHYAPFPGVYMLHCHNLIHEDHDMMAAFNV 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLSMDPMLDMMGMQMLMEKYGDQAMAGMDHSQMMGHMGHGNMNHMN--HGGKFDFHHAN- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAKRYNADGTL---FSTNGEVSSFWGDVIQVNGQPWPMLNVQPRKY-RFRELNAAVSRSF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLPGAD-GLGVEPEFDNTDKVMRFVVDEVLES---PDT-SEVPANLRDVPFPEG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYYYPNRQAARMLWYHDHAMSITAENAYMGQAGVYMIQDPAEDALNLPSGYGEFDIPLVL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYNGNLLGPAVKLQRGKAVTVDIYN - - QLTEETTLHWHGLEVPGEVDGGPQGIIPPGGKR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAAHRAGWKDTVKVEGNVSEVLVKFNHDAPKEHAYMAHCHLLEHEDTGMMLGFTV 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ~ † KINGQAFD ~ ~ MNKPMFAAAKGQYERWVISGVGDMMLHPFHIHGTQFRILSEN ~ ~ ~ GKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QWTINGVTFSDVENRLLRNVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSRSTARGVE 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLPVSQMGMAIAP-FDKPHPVMRIQPIAISASGALPDTLSSLPA----LPSLEGLTVRKL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LNFATSDNR----PLYVIASDGGLLPEPVKVSELPVLMGERFEVLVEVND--NKPFDL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDKKFSADGQIDYQLDVMTAAVGWFGDTLLTNGAIYPQ-HAAPRGWLRLRLLNGCNARS- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYTLMYDQPAATCWFHPHQHGKTGRQVAMGLAGLVVIEDDEILKLMLPKQWGIDDVPVIV 185
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29.7%;
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                                                                            Score 402.5; DB 2,
Pred. No. 6.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 412.5;
Pred. No. 1.:
                                                                                                                                                                                                                                                                                                                                                                                                                                            K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; C. Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GNWDPANPTDDETFTFGRANG 405
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probable cell division protein suff [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0083
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarradga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre
                                                                                                            Qy
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C;Genetics:
A;Gene: sufI
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A;Molecule type: DNA
A;Residues: 1-474 <KUR>
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A; Title: Genome sequence of Yersinia pestis, the causative A; Reference number: AB0001; MUID:21470413; PMID:11586360
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AD0083
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                                  QAGVYMIQDPAEDALNLPSGYGEFDIPLVLTAKRYNADGTLFSTNGEVSSFWGDVIQVNG
                                                                                                                                                                                           NTGEDILYYEMEIRPFSHQIYPDLEPANMYGYDGMSPGPTIIVPRGTESVVRFVNSGENT
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                                                                                                              SPNSVHLHGSESRAPFDGWAEDTTQPGEYKDYYYPNRQAARMLWYHDHAMSITAENAYMG
                                                                                                                                                        RRGQP-LFLTLQ---RAHWAFSGNKKAAVWGINGMYLGPTVRVFNGDD--VKLIYSNRLT
                                                                                                                                                                                                                                  AAGLA-LGAGSLPLRAQAS-STQQPQ-----ES
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LAGMWLVEDAVSKAMPLPSHYGVDDFPLIIQDKRLDNFGVPEYNPPAKGGFVGDTLLVNG
                                                                           EPVSMTISGLQVPGTLMGGEARMIRPGEDWSPVLPVRQPAANCWYHANTPNRMAPHVYNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IHLVDFRVLSRSTARGVEP-YEAAGLKDVVWL--ARREVVYVEAHYAPFPGVYMLHCHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMGNMNHGGKFDFHNAN---FINGQVFD--MNKPMFAAQKGRHERWVISGVGDMMLHPFH
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                                                                                                                                                                                                                                                                                                               136;
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                    10.9%; Score 339.5; DB 2; 27.6%; Pred. No. 1.7e-16;
                                                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN:CAC89527.1;
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Oy 130 SPNSVH Db 97 ENVSMT OY 190 QAGVYM	A; Experimental source: C; Genetics: A; Gene: ECs3901 Query Match Guery Match Best Local Similarity Matches 131; Conser Qy 10 ALGLAVIGGSVPL Db 11 ASGIALCAGAVPL Qy 70 NTGEDILYYEMEI Qy 70 RRGQPLFMTV	ESULT 91116 ppress ;Specie ;Date: ;Access ;Hayash asawara NA Res. ;Title: ;Tefere ;Access ;Access	Qy 250 QPWPM Db 218 AQSPF Qy 310 LYISM Qy 310 LYISM Qy 348 EFDNT Qy 348 EFDNT Db 332 LVI Db 332 LVI Db 371 WDMNF Qy 467 YEAAG Qy 418 -EDRG
SPNSYLHKSFSRAFEDGWAEDTTOPGEYKDYYVNY :	ntal source: strain O157:H7; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	imported hia coli hia coli #sequenc mo, K.; O laga, T.; 2001 2001 2002 2001 2002 2003	QPWPMLNVQPRKYFFFLWAAVSRSFALYLATSED :
YKDYYYPNRQA YKDYYYPNRQA	substrain RIMD substrain RIMD substrain RIMD a 322; DB 2; NO 2.9e-15; itsmatches 204; itsmatches 204; itsmatches 101; itsmatch	ichia coli (str. 18-Jul-2001 #t. ; Kurokawa, K.; ; Shiba, T.; Ha nterohemorrhagi 231; PMID:11258	SETR RNLP
ARMLWYHDHAMSTTAENAYMG 189	Length 470; Length 470; Lindels 114; Gaps YEVPLEIPPLKAPNTVPNP 69 -QOPLEVPPLLES 42 IVPRGTESVVRFVNSGENT 129 RVWKGDDVKLIYSNRLT 96	subst. -Jul*; okoyan inagav	DSETRLFFQVIAADGGLLEGPVDTDT 309PLYVVASDQGFLPAPVAVQQ 271 -RNLPGADGL
5 8 9 9 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	20 21 2	57:	29 77 31 30 66

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Suppressor of fts1 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 **sequence_revision 16-Feb-2001 **text_change 14-Sep-2001
C;Accession: E85961
C;Accession: E85961
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Ntture 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-470 <STO>
A;Cross-references: GB:AE005174; NID:g12517586; PIDN:AAG58153.1; GSPDB:GN00145; UWGP:A:Experimental source: strain O157:H7, substrain EDL933
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                                   RGVEPY-EAAGLKDVVWL---ARREVVYVEAHYAPFP 494
                                                                                                                                                        ANGQ-WTINGVTFSDVENRLLRNVPRDTVEIWRLENNSNGWTHPVHIHLVDFRVLSRSTA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPWPMLNVQPRKYRFRFLNAAVSRSFALYLATSEDSETRLPFQVIAADGGLLEGPVDTDT
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NGAMPFPEDRGWKDTVWVDGQVELLVYFGQPSWAHFP 445
                                                                                                    INGQLWDVNRI---DV-----TAQQGTWERWTVRADE---PQAFHIEGVMFQI---RNV 408
                                                                                                                                                                                                         GLLPLV--TDSLPMRLLPTEIMAGS-----PIRSRDISLGD----DPG---
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G65088
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A;Title: Characterization of the Escherichia coli gene for 1-acyl-sn-glycerol-3-phospha
A;Reference number: 820459; MUID:92212294
A;Accession: 820461
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A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M63491; NID:g147296; PIDN:AAA24398.1; PID:g147299
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A;Residues: 1-89 <COL>
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Best Local Similarity 25.3
Matches 131; Conservative
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;Species: Escherichia coli
;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
;Accession: G65088; S20461
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NGAMPFPEDRGWKDTVWVDGQVELLVYFGQPSWAHFP 445
                                                                                                              INGQLWDVNRI---DV----TAQQGTWERWTVRADE---PQAFHIEGVMFQI---RNV 408
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hypothetical prote
spore coat protein
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301 301

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300 300 360

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61 61 21 21 21 81		A;Status: preliminary A;Molecule type: DNA A;Residues: 1-572 <koi1> A;Cross-references: GB:D14081; NID A;Cross-references extracted from NC A;Accession: A48521 A;Status: preliminary A;Molecule type: mRNA; protein A;Residues: 1-572 <koi2> A;Cross-references: GB:D14081; NID A;Note: sequence extracted from NC C;Keywords: oxidoreductase</koi2></koi1>	ISULT 1 18521 Lirubin oxidase (EC 1.3.3.5) - Species: Myrothecium verrucaria Date: 16-Feb-1994 #sequence_rev. Accession: B48521; A88521 - Roikeda, S.; Ando, K.; Kaji, H. Biol. Chem. 268, 18801-18809; Title: Molecular cloning of the Reference number: A48521; MUID: Accession: B48521; MUID:	201.5 199.5 199.5 197.5 197.5 197.1 197.1 198.1 191.1 191.1 191.1 189.5 189.5 189.5 189.5
NPVNGQEJ NPNSVHLI NPNSVHLI NPNSVHLI NPNSVHLI NPNSVHLI NPNSVHLI NAGLYMLJ	llarity Conserva BAAALSLLF	Lnary DNA CKOI13 CKOI13 SS: GB:I SS: GB:I S21 Lnary Lnary MRNA; I SK: GB:I SS: GB:I SC: CKOI13 CKOI1	e (EC 1) necium v 194 #sec 1521; A48 160, K.; 188 161; 188 17; 188 181; 188	00000000000000000000000000000000000000
	100.0% 100.0% 7ative /ATIVE // IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	D14081; bed fro protein protein po14081; ced fro	m verrucaria sequence_revision A48521, M.; Inou K.; Kaji, H.; Inou 801-18809, 1993 oning of the gene 48521; MUID:933667	580 548 551 529 524 624 619 629 636 636 636 636 631
PAFI PAFI PAFI PALNI	.08; .08; .VQAS	om L) - aria _rev _rev the	000000000000000000000000000000000000000
THOUYPDLGSAD	Score 3067; Pred. No. 1 Pred. No. 1 ; Mismatche: PVPETSPATGHLF! PVPETSPATGHLF!	:g436236; BI backbor :g436236; BI backbor	ungus (My sion 18-N sion 10-N Inoue, T 993 gene for 3366794	F84828 518746 518752 502752 701240 701240 A36962 A82528 H82528 F82528 S56214 556214 552253 S52253 S472493 S472493 S49120 C8284 B1GNMENTS
PRLTYTNPVNGQEIWYYEVEIKPFTHQYYPDLGSADLVGYDGMSPGPTFQVPRGVETVVR	tch 100.0%; Score 3067; DB 2; Length 572; al Similarity 100.0%; Pred. No. 1.8e-217; 572; Conservative 0; Mismatches 0; Indels 0; G: Mismatches 0; Indels	66.1; PID:g4567 6730, NCBIP:136 66.1; PID:g4567 6728, NCBIP:136	verrucaria) text_change 2 s.; Takeuchi oxidase from	probable laccase laccase (EC 1.10. probable laccase (EC 1.10. probable membrane laccase laccase laccase (EC 1.10. probable membrane laccase (EC 1.10. copper resistance
120 120 180 180 240	aps 0;	10 732) 732) 729)	1-Jul-2000 , K.; Samejima, Myrothecium ver	laccase ([EC 1.10.3] laccase (EC 1.10.3] [EC 1.10.3] [EC 1.10.3] [EC 1.10.3] membrane like prote selstance se precur [EC 1.10.3]

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Spore coat protein (outer) cotA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: D5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: F69604; A27393; S02538
C;Accession: F69604
A;Enrich, S.; Broughl, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Chc
A; Ehrlich, S.; Enritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Yoshikawa, H.F.; Zumstein, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference, number: A69580; MUID:98044033
A;Reference number: A69580; MUID:98044033
A;Steference number: A69580; MUID:98044033
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A;Title: Identification of the promoter for a spore coat prot A;Reference number: S02538; MUID:88286730
A;Accession: S02538
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A; Residues: 1-37 < DON>
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A; Residues: 1-513 <KUN>
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                                                  Best Local Similarity Matches 177; Conserv
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  49 FTVPLPIP----PVKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLGSADLVGYDGMS 104
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                                                    Conservative
                                                                            23.2%;
                                                                                                                                                                                                                                                           protein is responsible for the characteristic brown
                                               77;
                                                                          Score 713; DB 2;
Pred. No. 1.5e-44;
                                                       Mismatches
                                                                                                  Length 513;
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Best Local Similarity
Matches 168; Conserv
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|---FVDALPIPDTLKPVQQ---
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                                                                              - VTETPKVGTTEIWSIINPTRG-THPIHLHLVSFRVLDRRPFDIARYQESGELSYTGPAV
                                                                                                                   LLANVP-VGTVERWELINAGNGWTHPIHIHLVDFKVISRTSGNNAR------
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hypothetical protein F19Gl0.5 - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C.Accession: B86364
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White,
C.Hin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
A;Authors: M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Ritle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719 A; Molecule type: DNA
A; Residues: 1-568 <STO>
A; Cross-references: GB:
C; Genetics: A; Reference number: A86141; A; Accession: B86364 A; Map position: 1 A;Status: preliminary GB:AE005172; NID:g2462832; PIDN:AAB72167.1; GSPDB:GN00141 C.J.; Federspiel, N.A.; Kaul, S.; White, Conway, A.B.; Conway, A.R.; Creasy, T.H.; æ.; Ξ., E.; Kim, 0

99 77

GYDGMS-----PGPTFQVPRGVETVVRFIN-----

-DMPRLYGFNSVHG

----IIKPASLQIGMFSTKWKFHRDLPATPVF

---NAEAPNSVH 132

METVPLPIPPVKQPRLTVTNPVNGQEIWYYEVEIKPETHQV-----YPDLGSADLV 98

Mismatches

180;

Gaps

27;

Conservative

16.5%; Score 29.3%; Pred. 70;

506; DB 2; No. 2.8e-29;

Length 568 Indels 156;

AY-GTSRSKATVPGPTIETVYGVDTYVTWRNHLPKSHILPWDPTISPATPKHGGIPTVVH

29 48

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spore coat protein-like protein, 24980-21957 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96734
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
A. Hulzar, L.
Nature 408, 816-820, 2000
A.A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.;Arther, Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.;Accession: G96734
A.;Acteres. Tooligneer.
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A; Residues: 1-591 <STO>
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                                                                                                                                                                                                                                                                                                             A;Map
                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE005173; NID:g6714313; PIDN:AAF26006.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                        Query Match
Best Local S
Matches 156
                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                          position:
    143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453
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                                                  125
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                                                                                              84
                                                                                                                                                                                        Local Similarity
nes 156; Conserv
                                                                                                                                                                                                                                                                                                                                     F23N20.3
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GGIPTVVHLHGGIHEPTSDGNADSWFTAGFKETGSKWTKKTTHYVNKQQPGNMWYHDHAA 202
                                                                                                                                LAAGLEEFKECMTKONDAVKCQISKYARGKKTAVTAHERGWKNVFKMMPGHVTRILVRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEAPNSVHLHGSFSRAAFDGWAED-----ITEPGS---FKDYYYPNRQSARTLWYHDHAM 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YA-----PF----PGVYMFHCHNLIHEDHDMM 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GNNA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFADVQNRLLAN-----VPV------GTVERWELINAGNGWTHPIHIHLVDFKVISRTS- 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSGLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNLGGSIGGIGTDTDY------:347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRQQAGLYMLTDPA-EDALNLPSGYGEFDIPMILTSKQYTANG----NLVTTNGELNSFW 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \texttt{LHGGIHEPTSDGNA-DAWFTAGFRETGPKWTKTTLHYENKQQPGNMWYHDHAMGLTRVNL} ~ \ref{thm:prop} 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHGSFSRAAFDGWAEDITEPGSFKD-----YYYPNRQSARTLWYHDHAMHITAENA 183
                                                                                            DLPATPVFAY-GTSKRSATVPGPTIEAVYGVDTYVTWRNHLPLHHILPWDPTISPAIPKH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVNEENGKVMKFII-NNESEDDTCTIPKKL--INYPNADVSNAVLTRY----ISMYEYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSAYLSKPVMTKSILLSPSEIVDVVVDFYKSPSRTVVLAN------DAPYPYPSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GDVIHVNGQPWPFKNVEPRKYRFRFLDAAVSRSFGLYFADTDAIDTRLPFKVIAS 293
                                                                                                                                                                                        Conservative
                                                                                                                                                                                   15.3%; Score 470; DB 2; 1
29.6%; Pred. No. 1.3e-26;
tive 66; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GRRETVVVEAH
                                                                                                                                                                                                                                    Length 591;
                                                                                                                                                                                      Indels 122;
                                                                                                                                                                                   Gaps
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A;Title: Genome sequence of Yersinia pestis, the causative A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AC0414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable exported protein YPO3409 [imported] - Yersinia pestis (strain CO92
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AC0414
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A;Molecule type: DNA
A;Residues: 1-533 <KUR>
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Best Local Similarity
Matches 141; Conserv
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248
                                     277
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                                                                      TLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSKQYTANGNL
                                                                                                                                                                                                                           AIRLQRGKAVTIDITNALPEATTVHWHGLEIPGEVDGGPQALIQPGAKRQVTFAVEQPAA
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                                                                                                                                                TCWFHPHTHSKTGHQVAMGLGGLVLIDDSDSETLPLPKQWGVDDIPVILQDK------L
                                                                                                                                                                                                                                                              TFQVPRGVETVVRFINNAEAPNSVHLHGSFSRAAFDGWAEDITEPGSFKDYYYPNRQSAR 167
                                                                                                                                                                                                                                                                                                   PLPIPPLLQPDANGKINL-NIQTGSVVWL-----PST-----ATQTWGYNGNLLGP
                                                                                                                                                                                                                                                                                                                                       PLPIPPVKQP----RLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLGSADLVGYDGMSPGP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLEQTALVKSEEFIECMTKRNDAVKCEISKYARGNKTAVTVHERGWKNVFKMMPGHVTKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLYINGLPY----NAPVTETPKIGTSEFKSLMLTIMKVWEVINLTED-NHPLHIHLGLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WT-INGVAFADVQNRLLANVP-VGTVE-----RWELINAGNGWTHPIHIHLVDFK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFIVVGSDSAYLAKPVSTKSVLLAPSEIVDVLVDFSKSTSKTAILANNAPYPYPSGDPVT
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-ALSDGRPMYVIASDGGLLAEPVVVRELPILMGERFEVLVDTRD--GQSLDLVTLPV
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                14.3%;
26.1%;
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                                                                                                           --SFWGDVIHVNGQPWPFKNVEPRKY-RFRFLDAAVSRSFGLYF
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                                                                                                                                                                                                                                                                                                                                                                          70;
                                                                                                                                                                                                                                                                                                                                                                                                Score 437.5; DB 2;
Pred. No. 2.7e-24;
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Indels 121;
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AC3582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable blue-copper protein yack precursor [imported] - Brucella melitensis (strain 16% C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: AC3582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: BMEII0580
A;Map position: I
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A;Residues: 1-494 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53822.1; PID:g17984756; GSPDB:GN00191
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                                          ----HLMRFTV-DPALEGRVAKPPVSLDGPAAPDEKLSVQRRSFFFDERMAENMKLMMRQ 339
                                                                                                                                  LLVIASDGGFISQPVSIEQLTISPGERYEVLVDFSN--GEAVDLVTYGDNGSGDGL----
                                                                                                                                                                           FKVIASDSGLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNLGGSIGGIGTDTDY
                                                                                                                                                                                                                        PDIMDLIHGFRGDWLIVNGAIAPEARVPAAMVRLRLLNGANARNFHIRFAD------GRP
                                                                                                                                                                                                                                                                                                                                                       YHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSKQYTANGNLV-- 228
                                                                                                                                                                                                                                                                                                                                                                                                 MSG-ESVTLSVENAMDEETTLHWHGLFVPSHLDGGPHNVIAPGAKWEPKVAVNQPASFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRGVETVVRFINNA-EAPNSVHLHGSFSRAAFDGWAEDITEPGSFKDYYYPNRQSARTLW 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLPLPPLVEPDAS------GIVRLKVQKGRHS-FAKGSTAASAGINGAYLGPLVRL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGKPPAEHRRGWKDIVRVEGARSEILVRFNYLAPASTPYMAHCHLLEHEDTGMMLGFTV
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                                                                                     DNTDKVMRFVVADDTTQPDTSVVPANLRDVPFPSPTTNTPRQFRF--
                                                                                                                                                                                                                                                   -TTNGELNSFWGDVIHVNGQPWPFKNVEPRKYRFRFLDAAVSRSFGLYFADTDAIDTRLP 287
                                                                                                                                                                                                                                                                                                              FHPHLHGHTARQAHMGIAGLMIVRDGKDAERGLPETYGVDDLPLVLQDRR-VIEGDAVYA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.1%; Score 403; DB 2; I al Similarity 26.4%; Pred. No. 8.3e-22; 137; Conservative 71; Mismatches 214;
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probable copper-binding protein yack - Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change C; Accession: C64735; S45200 R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; B. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID: 97426617 A; A; Accession: C64735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE000121; GB:U00096; NID:g1786306; PIDN:AAC73234.1; A;Experimental source: strain K-12, substrain MG1655 R;Fujita, N. submitted to the EMBL Data Library, January 1994 A;Reference number: S45181 A;Accession: S45200
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C;Keywords: c
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A; Residues: 1-516 <BLAT>
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Best Local Similarity
Matches 136; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 GYDGMSPGPTFQVPRGVETVVRFINNAEAPNSVHLHGSFSRAAFDGWAEDITEPGSFKDY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYNGNLLGPAVKLQRGKAVTVDIYNQLTEETTLHWHGLEVPGEVDGGPQGIIPPGGKRSV 127
                                                                                                                                                                                                                            RNLGGSIGGIGTDTDYDNTDKVMR---FVVADDTTQPDT-SVVPANLRDVPFPSPTTNTP 387
                                                                                                                                                                                                                                                                                                     FGLYFADTDAIDTRLPFKVIASDSGLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIEL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YYPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTS 218
                                           TINGVAFADVQNRLLANVPVGTVERWELINAGNGWTHPIHIHLVDFKVISRTSGNNARTV 459
                                                                                                                                                                                                                                                                             --LNFATSD----NRPLYVIASDGGLLPEPVKVSELPVLMGERFEVLVEVND--NKPFDL
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  KINGQAFD--MNKPMFAAAKGQYERWVISGVGDMMLHPFHIHGTQFRILS---
                                                                                                                                                                                   VTLPVSQMGMAI-APFDKPHPVMRIQPIAISASGALPDTLSSLPA-----LPSLEGLTV 348
                                                                                                                                                                                                                                                                                                                                                                            KKFSADGQI----DYQLDVMTAAVGWFGDTLLTNGAIYP-QHAAPRGWLRLRLLNGCNARS
                                                                                                                                                                                                                                                                                                                                                                                                                     KQYTANGNLVTTNGELN-----SFWGDVIHVNGQPWPFKNVEPRKY-RFRFLDAAVSRS 271
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                                                                                         RKLQLSMDPMLDMMGMQMLMEKYGDQAMAGMDHSQMMGHMGHGNMNHMNHGGKFDFHHAN 408
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RESULT 9

690644
hypothetical protein ECs0127 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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A;Cross-references: GB:AE000724; NID:g2983585;
A;Experimental source: strain VF5
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C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: C70397
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C; Species: !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSVHLHGSFSRAAFDG---WAEDITEPGSFKDYYYPNRQSARTLWYHDHAMHITAENAYR 185
                                                                                                                                                                                                   LERSLGPLRAT----DLGWKDTVIVAPMETVRIAVDMSHPYNEHQIYLLHCHILEHHDEG 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNLTPNPYMDVERKIYRERILNGSNARPYRL-----ALLRGNQRMREWVIGVEGGLLDT 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNGQPWPFKNVEPRKYRFRFLDAAVSRSFGLYFADTDAI---DTRLPFKVIASDSGLLEH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQAGLYMLTDPAEDALN--LPSGYGEFDIPMILTSKQYTANGNLVTTNGELNSFWGDVIH 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIIHWHGFRAPWKSDGHPYYAVKDGETYSYPDFTIIDRSG--TYFYHPHPHGRTGYQVYY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGQRV---SITAKWTTLEVIPG-KSTDMLVYEIDNEYNPVIFLRKGQTFSADFVNNSGED 114
                                                                                                                               ANAMW
                                                                                                                                                                 MMAAF
                                                                                                                                                                                                                                                                         RMVFTINGETWEDGYANPQDINNPKVLFEQNNGDVVIIEYVN-NTGMYHPMHIHGFQFQV
                                                                                                                                                                                                                                                                                                                                                                                                              PKEVNEILVAPGERIDILVDFRDASVNDVIKLYNFPHNLIGMGMIGMRMGMGMERGMGMG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PADTSLLYISMAERYEVVFDFSDYA-GKTIELRN-----LG-GSIG------------G 340 : }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGQEIWYYEVEIKPFTHQVYPDLGSADLVGYD-GMSPGPTFQVPRGVETVVRFINNAEAP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPYESGLKDVVWL-GRRETVVVE-AHYAPFPGVYMFHCHNLIHEDHDMMAAF
                                                                                                                                                                                                                                                                                                              QFRFGRTGPTWTINGVAFADVQN-RLLANVPVGTVERWELINAGNGWTHPIHIHLVDFKV 447
                                                                                                                                                                                                                                                                                                                                                NGMNMDMGMADNSEFEVMEFRVTKDSAY-DKS-IPQRLSEVT-PINTDGAQVQRITLGMR 403
                                                                                                                                                                                                                                                                                                                                                                                    IGTDTDY----DNTD-KVMRFVVADDTTQPDTSVVPANLRDVPFPSPT-----TNTPR 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLAGMIIIEDEDEDNLKQALDLEYGVIDIPLIIQDKTFDSSGQLVYNPMGHMGFWGDTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146;
                                                                                                                                                                                                                                     ISRTSGNNARTVMPYESGLKDVVWLGRRETV---VVEAHYAPFPGVYMFHCHNLIHEDHD 504
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30.1%;
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Pred. No. 1.4e-21;
72; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAC07157.1;
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K;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90644
A;Status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-516 < HAY>
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Matches 13
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                                    460 MPYESGLKDVVWL-GRRETVVVE-AHYAPFPGVYMFHCHNLIHEDHDMMAAF
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                                                                                                                                                                                                                                                                                                                                                    244 -- LNFATSD---- NRPLYVIASDGGLLPEPYKVNELPYLMGERFEVLVEVND--NKPFDL
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463 AAHRAGWKDTVKVEGNVSEVLVKFNHDAPKERAYMAHCHLLEHEDTGMMLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 TLNVDQPAATCWFHPHQHGKTGRQVAMGLAGLVVIEDDEILKLMLPKQWGIDDVPVIVQD 187
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                                                                                                                               TINGVAFADVQNRLLANVPVGTVERWELINAGNGWTHPIHIHLVDFKVISRTSGNNARTV 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYNGNLLGPAVKLQRGKAVTVDIYNQLTEETTLHWHGLEVPGEVDGGPQGIIPPGGKRSV 127
                                                                                        KINGQAFD--MNKPMFAAAKGQYERWVISGVGDMMLHPFHIHGTQFRILS----ENGKPP
                                                                                                                                                                              RKLQLSMDPMLDMMGMQMLMEKYGDQAMVGMDHSQMMGHMGHGNMNHMNHGGKFDFHHAN
                                                                                                                                                                                                                          RQFR--
                                                                                                                                                                                                                                                                VTLPVSQMGMAI-APFDKPHPVMRIQPIAISASGALPDTLSSLPA-----LPSLEGLTV
                                                                                                                                                                                                                                                                                                       RNLGGSIGGIGTDTDYDNTDKVMR---FVVADDTTQPDT-SVVPANLRDVPFPSPTTNTP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                        KKFSADGQI----DYQLDVMTAAVGWFGDTLLTNGAIYP-QHAAPRGWLRLRLLNGCNARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYDGMSPGPTFQVPRGVETVVRFINNAEAPNSVHLHGSFSRAAFDGWAEDITEPGSFKDY 158
                                                                                                                                                                                                                                                                                                                                                                                             FGLYFADTDAIDTRLPFKYIASDSGLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQYTANGNLVTTNGELN-----SFWGDVIHVNGQPWPFKNVEPRKY-RFRFLDAAVSRS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
135; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.0%; Score 398; DB 2; 28.6%; Pred. No. 2.1e-21; tive 59; Mismatches 192
                                                                                                                                                                                                                          ----FGRTG-----
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RESULT 10 G85495

hypothetical protein yack [imported] - Escherichia coli (strain O157:H7, substrain ED C;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: G85495
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85495
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-516 <STOO
A;Cross: references: GB:AE005174; NID:g12512835; PIDN:AAG54427.1; GSPDB:GN00145; UWGP: A;Cene: yack

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C;Geneti
A;Gene:
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A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonelia enterica serov A:Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable multicopper oxidase precursor [imported] - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AF0523
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A; Residues: 1-536 <PAR>
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                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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                                                                                                                                                                     Query Match
Best Local
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Best Local
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              TFTPQQRAATCWIHPHKHGKTGRQVAMGLAGLVLIEDDEIRKLRLPKQWGIDDVPVIIQD 187
                                              YYPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTS 218
                                                                                 GYNGNLLGPAVQLHKGKSVTVDIHNQLAEDTTLHWHGLEIPGIVDGGPQGIIPAGGTRTV 127
                                                                                                                 GYDGMSPGPTFQVPRGVETVVRFINNAEAPNSVHLHGSFSRAAFDGWAEDITEPGSFKDY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAHRAGWKDTVKVEGNVSEVLVKFNHDAPKERAYMAHCHLLEHEDTGMMLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPYESGLKDVVWL-GRRETVVVE-AHYAPFPGVYMFHCHNLIHEDHDMMAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINGQAFD--MNKPMFAAAKGQYERWVISGVGDMMLHPFHIHGTQFRILS----ENGKPP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TINGVAFADVQNRLLANVPVGTVERWELINAGNGWTHPIHIHLVDFKVISRTSGNNARTV 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTLPVSQMGMAI-APFDKPHPVMRIQPIAISASGALPDTLSSLPA-----LPSLEGLTV 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LNFATSD----NRPLYVIASDGGLLPEPVKVNELPVLMGERFEVLVEVND--NKPFDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLNVDQPAATCWFHPHQHGKTGRQVAMGLAGLVVIEDDEILKLMLPKQWGIDDVPVIVQD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYNGNLLGPAVKLQRGKAVTVDIYNQLTEETTLHWHGLEVPGEVDGGPQGIIPPGGKRSV 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQYTANGNLVTTNGELN-----SFWGDVIHVNGQPWPFKNVEPRKY-RFRFLDAAVSRS 3/71
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                                                                                                                                                       131;
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26.7%;
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                                                                                                                                                 Score 398; DB 2;
Pred. No. 2.2e-21;
55; Mismatches 201
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Pred. No. 2.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
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                                                                                                                                                                                 Length 536
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probable cell division protein sufI [imported] - Yersinia pestis (strain CO92)
C;Speckes: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AL590842; PIDN:CAC89527.1; PID:g15978763; GSPDB:GN00175 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: AB0001; A; Accession: AD0083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, I.M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
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A; Residues: 1-474 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Genome sequence of Yersinia pestis, the causative A; Reference number: AB0001; MUID:21470413; PMID:11586360
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Best Local Similarity
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TLQLSD
                                                                                                                                                  PMILTSKQYTANGNLYTTNGELNSFWGDVIHVNGQPWPFKNVEPRKYRFRFLDAAVSRSF 272
                                                                                                                                                                                                                                                                                                         KKAAVWGINGMYLGPTVRVFNGDDVKLIYSNRLTEPVSMTISGLQVPGTLMGGEARMIRP 123
                                                                                                                                                                                                                                                                                                                                                        GSADLYGYDGMSPGPTFQYPRGYETVVRFINNAEAPNSVHLHGSFSRAAFDGWAEDITEP 152
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                                                    GLYFADTDAIDTRLPFKVIASDSGLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELR 332
                                                                                                   PLIIQDKRLDNFGVPEYNPPAKGGFVGDTLLVNGAQSPFVEVSRGWVRLRLLNASNARRY
                                                                                                                                                                                                      GEDWSPVLPVRQPAANCWYHANTPNRMAPHVYNGLAGMWLVEDAVSKAMPLPSHYGVDDF 183
                                                                                                                                                                                                                                                     GSFKDYYYPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDI 212
                                                                                                                                                                                                                                                                                                                                                                                                         GSLPLRAQASSTQQPQ----LPVPPLLESR-----RGQPLFL----TLQRAHWAFSGN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHLFKRVAQISPQYPMFTVPLPIPPVKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDL 92
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  GRPLYVVASDQGFLPAPVAVQQLSLAPGERREVVIDMSQ--GNEVSI-
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Pred. No. 1.
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Dougan, G
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cyspecies: Escherichia coli
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A;Molecule type: DNA
A;Residues: 1-470 <HAY>
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AHYAPFPGVYMFHCHNLIHEDHDMMAAFNATVLP
                             TVRADE--PQAFHIEGVMFQI-----RNVNGAMPFPEDRGWKDTVWVDGQVELLVYFGQ 438
                                                                                                                                                                                                                              VRLRLLNASNSRRYQLQMSD-----GRPLHVISGDQGFLPAPVSVKQLSLAPGERREIL
                                                                                                                                                                                                                                                                                               KSLPIPNHYGVDDFPVIIQDKRLDNFGTPEYNEPGSGGFVGDTLLVNGVQSPYVEVSRGW
                                                                                                                                                                                                                                                                                                                                                          PGPLMGGPARMMSPNADWAPVLPIRQNAATLWYHANTPNRTAQQVYNGLAGMWLVEDEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVQASPVPETSPATGHLFKRVAQISPQYPMFTVPLPIPPVKQPRLTVTNPVNGQEIWYYE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPQAFHIQGVSFLVKS----VNGAAAMAEDRGWKDTVWV
                                                              LINAGNGWTHPIHIHLVDFKVISRTSGNNARTVMPY--ESGLKDVVWL-GRRETVVV--E, 481
                                                                                                PLVTDSLPMRLLPTEIMAGSPIRSRDISLGDDPGINGQLW-DV-NRIDVTAQQGTWERW-
                                                                                                                               PANLRDVPFP-SPT---TNTPRQFRFGRTGPTWTINGVAFADVQNRLLANVPVGTVERWE 426
                                                                                                                                                                VDMSN--GDEVSI--TCGEAASI-----VDRIRGFFEPSSILVSTLVLTLRP-TGLL
                                                                                                                                                                                               FDFSDYAGKTIELRNLGGSIGGIGTDTDYDNTDKVMRFVVADD-----TTQPDTSVV
                                                                                                                                                                                                                                                                                                                              DALNLPSGYGEFDIPMILTSKQYTANGNLYTTNGELNSFWGDVIHVNGQPWPFKNVEPRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALCAGAVPLKASAAGQ------QQPLPVPPLLESR------RGQPL-FMT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Makino, K.; Ohnishi, M.;
Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.2e-15;
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Shiba, T.; Hattori, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-470 <STO>
A;Cross-references: GB:AE005174; NID:g12517586; PIDN:AAG58153.1;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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Best Local Similarity
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                                                            PSWAHFP--FYFNSQTLEMADRGSIGQLLVNPVP
                                                                                           AHYAPFPGVYMFHCHNLIHEDHDMMAAFNATVLP
                                                                                                                                          LINAGNGWTHPIHIHLVDFKVISRTSGNNARTVMPY--ESGLKDVVWL-GRRETVVV--E
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                                                                                                                        TVRADE---PQAFHIEGVMFQI-----RNVNGAMPFPEDRGWKDTVWVDGQVELLVYFGQ
                                                                                                                                                                                     PLVTDSLPMRLLPTEIMAGSPIRSRDISLGDDPGINGQLW-DV-NRIDVTAQQGTWERW-
                                                                                                                                                                                                                  PANLRDVPFP-SPT---TNTPRQFRFGRTGPTWTINGVAFADVQNRLLANVPVGTVERWE
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25.9%;
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Pred. No. 1.2e-15;
2; Mismatches 234;
                                                                                                                                                                                                                                                                                                               --GRPLHVISGDQGFLPAPVSVKQLSLAPGERREIL
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sufI protein precursor - Escherichia coli (C.Species: Escherichia coli (C.

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Search completed: October 3, 2002, 10:55:35 Job time: 79 sec
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A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G65088
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A;Residues: 1-89 <COL>
A;Cross-references: GB:M63491; NID:g147296; PIDN:AAA24398.1; PID:g147299
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A.Title: Characterization of the Escherichia coli gene for 1-acyl-sn-glycerol-3-phospha
A.Reference number: S20459; MUID:92212294
A.Accession: S20461
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A;Experimental source: strain K-12, substrain MG1655
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A; Residues: 1-470 <BLAT>
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Matches 133; Conserv
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                                                                                                                                                  439 PSWAHFP--FYFNSQTLEMADRGSIGQLLVNPVP 470
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Database
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Maximum DB seq
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   score greater and is derived
Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution.
                                                                                                                                                     A_Geneseq_032802:*

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Matches 383
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(UNIL ) UNILEVER PLC.
(HIND-) HINDUSTAN LEVER LTD.
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                                                                                                                                                                     GLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNLGGSIGGIGTDTDYDNTDKVMR
dvenrllrnvprdtveiwrlennsngwthpvhihlvdfrvlsrst--
                                DVQNRLLANVPVGTVERWELINAGNGWTHPIHIHLVDFKVISRTSGNNARTVMPYE-SGL 466
                                                                                   FVVADDTTQPDTSVVPANLRDVPFP----
                                                                                                                                     gllegpvdtdtlyismaerwevvidfstfagqsidirnlpga-dglgvepefdntdkvmr
                                                                                                                                                                                                       sfwgdv1qvngqpwpmlnvqprkyrfrflnaavsrsfalylatsedsetrlpfqv1aadg
                                                                                                                                                                                                                       SFWGDVIHVNGQPWPFKNVEPRKYRFRFLDAAVSRSFGLYFADTDAIDTRLPFKVIASDS 295
                                                                                                                                                                                                                                                                         \verb|msitae| nay mgqagvymiqdpaedalnlpsgygefdiplvltakrynadgtlfstngevs|
                                                                                                                                                                                                                                                                                              MHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSKQYTANGNLVTTNGELN 235
                                                                                                                                                                                                                                                                                                                                             vvrfvnsgentspnsvhlhgsfsrapfdgwaedttqpgeykdyyypnrqaarmlwyhdha
                                                                                                                                                                                                                                                                                                                                                               VVRFINNAE--APNSVHLHGSFSRAAFDGWAEDITEPGSFKDYYYPNRQSARTLWYHDHA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                 VKQPRLTVTNPVNGQEIWYYEVEIKPETHQYYPDLGSADLVGYDGMSPGPTFQVPRGVET 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 65.5%; al Similarity 65.4%; 383; Conservative 7
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Pred. No. 2.8e-174;
1; Mismatches 110;
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                                                                                   ---SPTTNTPRQFRFGRTGPTWTINGVAFA 407
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Matches 383
                                                                                                                                                      The present sequence is a Stachybotrys chartarum phenol oxidising enzyme. The invention relates to detergent compositions comprising one comore surfactants and a phenol oxidising enzyme having at least 60% identity to the Stachybotrys chartarum phenol oxidising enzyme. Phenol oxidising enzymes may be used in the detergent, paper, pulp, textile and food industries. They are used for preventing the transfer of dyes in solution from one textile to another during detergent washing, or in modifying the colour associated with dyes and coloured compounds having different chemical structures, such as in pulp and paper bleaching, bleaching the colour of stains on fabric and in detergent and textile
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                     Claim 1; Fig 2; 46pp; English.
                                                                                                                                                                                                                                                                                                                             New detergent compositions comprising a phenol oxidizing enzyme useful in detergent or cleaning compositions, fiber treatment, processing, finishing or production, paper and pulp production, or in starch processing applications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stachybotrys phenol oxidase B; spoB; phenol oxidising enzyme; detergent; paper production; pulp production; textile; food industry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stachybotrys chartarum phenol oxidase B enzyme
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                MFKHTLGAAALSL-LFNSNAVQASPVP--ETSPATGHLFKRVAQISPQYPMFTVPLPIPP'57
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                                                    383; Conservative
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71; Mismatches
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FVVADDTTQPDTSVVPANLRDVPFP-----SPTTNTPRQFRFGRTGPTWTINGVAFA
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                                                                                                                                                                      gllegpvdtdtlylsmaerwevvidfstfagqsidirnlpga-dglgvepefdntdkvmr
                                                                                                                                                                                 GLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNLGGSIGGIGTDTDYDNTDKVMR
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AAB20097 standard; Protein; 583 ₿

AAB20097;

23-APR-2001 (first entry)

Stachybotrys chartarum phenol oxidase . B

pulp; Phenol paper; oxidising sing enzyme; textile; det detergent phenol oxidase ₩. spoB gene; bleach;

Stachybotrys chartarum

US6168936-B1.

22-SEP-1999; 99US-0401476

22-SEP-1999; 99US-0401476

(GEMV) GENENCOR INT

Wang

WPI; 2001-136715/: N-PSDB; AAF30028, 2001-136715/14. AAF20029.

RESULT
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XX Stac
XX Phen
XX Phen
XX US61
XX US61
XX US61
XX US61
XX US62-5
XX GEW
PA (GEW
PA (GEW
XX WPI;
DR N-PS
XX New
PT PUlf
PT Pulf
PT Tarr
XX Clai New phenol oxidizing enzyme, also useful pulp, textile or food industries, especia associated with dyes and coloured compour transfer applications useful in the detergent, paper and especially in modifying the colour compounds, as well as in anti-dye

Claim 1; Fig 2; 23pp; English

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RESULT
AAY69204
ID AAYF
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Phenol oxidizing enzyme; fungus; redox reaction; detergent; bleaching; fabric; pulp; paper; decolourisation; plant-derived food product; coloured compound; porphyrin; tannin; polyphenol; carotenoid;
                                                                                                      Amino acid
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 fungus Acremonium murorum. The enzyme has the CBS accession number 157.72. The enzyme catalyses redox reactions and is specific for molecular oxygen as the electron acceptor. The phenol oxidising enzy is specifically used in detergents for bleaching strains on fabrics, but also for bleaching pulp and paper and for decolourisation of plant-derived food products. The enzyme has a pH optimum in the alkaline to neutral range and can bleach a wide variety of coloured compounds, e.g. porphytins, tannins; polyphenols, carotenoids, anthocyanins and Maillard reaction products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 41-43; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phenol-oxidizing enzyme from Acremonium,
for bleaching stains on fabrics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIL ) UNILEVER NV.
(UNIL ) UNILEVER PLC.
(HIND-) HINDUSTAN LEVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anthocyanin; Maillard
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1998;
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361
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                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                   40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence represents a phenol oxidizing enzyme from the
                                                                                                   YPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSK
                                                                                                                                                                                                      2000-195101/17.
DB; AAZ61243.
            GIGTDTDYDNIDKVMREVVAD-DTTQPDTSVVPANLRDVPEPSPTTNT-PRQEREGRTGP
                                                   adedtripfqviasdsglleepvttsklvlsiaeryeiildfsdfegktielrn-epavg
                                                               DAIDTRLPFKVIASDSGLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNLGGSIG
                                                                                                                              QYTANGNLVTTNGELNSFWGDVIHVNGQPWPFKNVEPRKYRFRFLDAAVSRSFGLYFADT
                                                                                                                                                                                                                                                                                  AQISPQYPMETVPLPIPPVKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLGSADLVG
                                                                                                                                                                                                                                                                                                                                     TLGAAALSLLFNSNAVQASP-----VPE-----TSPATGHLFKRV 39
glgievnyddtdkvmrfnvaegplsspdtsvvpstlrdvpfpsststtidhsfrfartag
                                                                                                                                                     y pnaqagrfs wyhdhamhetaenayng qaggyiihd paeds 1g1psgygeydipliltsk
                                                                                                                                                                                                                                                                                                          ttalralalylslkgagampkfeldipeeeaaalaaiveddpandlqrrspand--lqrr
                                                                                                                                                                                                                                                                                                                                                              365;
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                                                                                                                                                                                                                                                                                                                                                                                                                             602 AA;
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                                                                                                                                                                                                                                                                                                                                                                          62.4%; Score 1913; 61.0%; Pred. No. 2
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1e-165;
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TWTINGVAFADVQNRLLANVPVGTVERWELINAGNGWTHPIHIHLVDFKVISRT----SGN

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                                                                                    The present sequence is that of the Bipolarius spicifera phenol oxidising enzyme. The invention relates to detergent compositions comprising novel phenol oxidising enzymes that have at Cleast 60% identity with the phenol oxidising enzyme of Stachybotrys Chartarum (see AAY95537), and which are obtained from a bacterium, yeast or non-Stachybotrys fungus, especially B. spicifera, Curvularia pallescens (see AAY95539) and Amerosporium atrum (see CC AAY95540). The phenol oxidising enzyme is capable of modifying the CC colour associated with dyes or coloured compounds, and can be used CC fabric and for anti-dye transfer in detergent and textile CC fabric and for anti-dye transfer in detergent and textile CC the absence or presence of an enhancer. Expression vectors and CC the cells comprising a nucleic acid encoding a phenol oxidising CC enzyme, methods for producing the phenol oxidising enzyme, and the constructing expression hosts are provided.
Query Match
Best Local Similarity
Matches 333; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIL)
                                                                   Sequence
                                                                                                                                                                                                                                                                                                                          Claim 8; Fig 3; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                   Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition
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23-JUN-1999;
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99US-0338723.
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            58.7%;
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Score 1799; DB 21;
Pred. No. 5.5e-155;
7; Mismatches 123;
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           New phenol oxidizing enzyme for modifying colors associated with or colored compounds, is obtained from fungus and is encoded by a nucleic acid comprising a specific nucleotide sequence
                                                                WPI; 2000-452191/39.
N-PSDB; AAA51315.
                                                                                                                                                             23-DEC-1998;
23-JUN-1999;
                                                                                                                                                                                                                                                         WO200037654-A2
                                                                                                                                                                                                                                                                                 Bipolaris spicifera
                                                                                                                                                                                                                                                                                                            Phenol oxidizing enzyme; colour; pulp; paper bleaching.
                                                                                                                                                                                                                                                                                                                                                   Bipolaris spicifera phenol oxidizing enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMSPGPTFQVPRGVETVVRFINNAEAPNSVHLHGSFSRAAFDGWAEDITEPGSFKDYYYP
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                                                                                                      Bodie EA;
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99US-0338723
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XX AAY9
XX IO-C
DT 10-C
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                              WO200039306-A2
                                                         Curvularia pallescens
                                                                                      Phenol oxidising enzyme;
                                                                                                                 Curvularia pallescens phenol oxidising enzyme
                                                                                                                                               10-OCT-2000
                                                                                                                                                                             AAY95539;
                                                                                                                                                                                                        AAY95539 standard; Protein;
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                                                                                                                                                                                                                                                                                                         ATV-FVDPMEELWQARPYELGEFQAQSGQFSVQAVTERIQTMAEYRPYA 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTDTDYDNTDKVMRFVVADDTTQPDTSVVPANLRDVPFPSPTTNTPRQFRFGRTGPTWTI 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tatrlpfqviasdagllthpvqtsdmyvaaaeryeivfdfapyagqtldlrnf-akangi
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                                                                                                                                                                                                                                                                                                                                       yeaaglkdvvwlgrhetvlveahyapwdgvymfhchnlihedqdmmaafdvtklqnfgyn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.7%; Score 1799; DB 21; Length 627; 62.9%; Pred. No. 5.5e-155; tive 67; Mismatches 123; Indels 6
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Best Local Sim
Matches 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compositions comprising novel phenol oxidising enzyme that have at least 60% identity with the phenol oxidising enzyme of Stachybotrys chartarum (see AAY9537), and which are obtained from a bacterium, yeast or non-Stachybotrys fungus, especially C. pallescens, Bipolarius spicifera (see AAY9538) and Amerosporium atrum (see AAY9530). The phenol oxidising enzyme of stachybotrys fungus, especially C. pallescens, Bipolarius spicifera (see AAY9538) and Amerosporium atrum (see AAY95540). The phenol oxidising enzyme in the colour association of the colour association and the colour association of the colour association association of the colour association associati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bipolarius spicifera (see AAY95538) and Amerosporium atrum (see AAY95540). The phenol oxidising enzyme is capable of modifying t colour associated with dyes or coloured compounds, and can be use for pulp and paper bleaching, for bleaching the colour of stains fabric and for anti-dye transfer in detergent and textile applications. It may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidising enzyme, methods for producing the phenol oxidising enzyme, and methods for constructing expression hosts are provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detergent composition comprising novel phenol oxidising enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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(UNIL ) UNILEVER PLC.
(HIND-) HINDUSTAN LEVER LTD
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23-JUN-1999;
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NGVAFADVQNRLLANVPVGTVERWELLINAGNGWTHPIHIHLVDFKVISRTSGNNARTVMP 461
                                                                               gtdddyantdkvmrfhvssqav-vdnsvvpaqlsqiqfpadktgidhhfrfhrtnsewri
                                                                                                                GTDTDYDNTDKVMREVVADDTTQPDTSVVPANLRDVPFPSPTTNTPRQFRFGRTGPTWTI 401
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99US-0338723
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Matches 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New phenol oxidizing enzyme for modifying colors associated with dyes or colored compounds, is obtained from fungus and is encoded by a nucleic acid comprising a specific nucleotide sequence
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23-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96763 standard;
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                                                                                                       GMSPGPTFQVPRGVETVVRFINNAEAPNSVHLHGSFSRAAFDGWAEDITEPGSFKDYYYP 161
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DB; AAA51316.
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99US-0338723
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                                                                                                                                                                                                                                                                                                                 58.5%;
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                                                                                                                                                                                                                                                                                                                 Score 1795;
Pred. No. 1
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l.3e-154;
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                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                         627;
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RESULT :
The present invention describes a detergent composition containing purified phenol oxidising enzyme derived from Stachybotrys. The presequence represents Stachybotrys chartarum phenol oxidising enzyme enzyme can be used to modify the colour of dyes and other coloured compounds (e.g. for use in pulp and paper bleaching also for removerable, e.g. food, tea, blood etc., from fabrics) and for preventing the presentation of the preventing that the preventing the prevention the preventing the preventing the prevention the prevention the prevention that the prevention the prev
                                                                                                                                                                                                                                                                                                                                    Detergent
to bleach
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N-PSDB; AAZ25727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Convents D, Wang C;
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22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                     composition containing stains and prevent dye
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                                                                                                                                                                                                                                                                                                                                                              Stachybotrys,
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                                           24-MAR-1998;
22-DEC-1998;
22-MAR-1999;
       Amory A,
                                                                                                                                       Stachybotrys
                                                                                                                                                        Phenol oxidase; enzyme; coloured compound; dye transfer prevention; fabric washing; stain bleaching; anti-dye transfer; detergent.
                                                                                                                                                                                      Stachybotrys phenol oxidase protein sequence
                                                                                                                                                                                                                           AAY39992;
                          (GEMV ) GENENCOR INT INC
                                                                                                    30-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPQYP-MFTVPLPIPPVKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLGSADLVGYD 101
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       Wang
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                                                                                 99WO-US06327
       Dhase P,
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60.3%;
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Pred. No. 3.1
       Lambrechts-Rongvaux
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RESULT 12
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the Stachybotrys chartarum phenol oxidase enzyme of the invention. The invention is used to modify a coloured compound and prevent dye transfer during fabric washing, or for stain bleaching or anti-dye transfer. It is useful in the detergent, paper and pulp, textile and food industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel enzyme for modifying dye-transfer -
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N-PSDB; AAZ27601, AAZ27602
                 Stachybotrys chartarum
                                                      Stachybotrys chartarum
                                                                          10-OCT-2000
                                                                                             AAY95537;
                                                                                                                AAY95537 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                   Phenol oxidising enzyme; detergent; bleaching
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                                                                                                                                                            TINGVAFADVQNRLLANVPVGTVERWELINAGNGWTHPIHIHLVDFKVISRTSGNNARTV
                                                                                                                                                                                                                                                                                                                                                         lindvgfadvnervlakpelgtvevwelenssggwshpvhihlvdfkilkrtggrg--gv
                                                                                                                                                                                                                                                                               gdedeyartlevmrfvvssgtve-dnsqvpstlrdvpfp-phkegpadkhfkfersnghy
                                                                                                                                                                                                                                                                                         pnvripfqviasdagllqapvqtsnlylavaeryeiiidftnfagqtldlrnv-aetndv
                                                                                                                                                                                                                                                                                                                                sppynllyrnalpippvkqpkmiitnpvtgkdiwyyeieikpfqqriyptlrpatlvgyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPQYP-MFTVPLPIPPVKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLGSADLVGYD 101
                                                                                                                                                                                                                        MPYES-GLKDVVWLGRRETVVVEAHYAPFPGVYMFHCHNLIHEDHDMMAAFNATVLPDYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                      phenol oxidising
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The present sequence is that of a phenol oxidising enzyme of Stachybotrys chartarum MUCL 38898. A claimed detergent composition comprises a phenol oxidising enzyme having at least 60% identity to the present sequence, and preferably obtained from a bacterium, yeast or non-Stachybotrys fungus, especially Bipolarius spicifera, C Curvularia pallescens or Amerosporium atrum (see AAY95538-40). The phenol oxidising enzyme is capable of modifying the colour associated with dyes or coloured compounds, and can be used for pulp and paper bleaching, for bleaching the colour of stains on the absence or presence of an enhancer. Expression vectors and the absence or presence of an enhancer. Expression vectors and the absence or presence of an enhancer. Expression vectors and constructing a nucleic acid encoding a phenol oxidising enzyme, methods for producing the phenol oxidising enzyme, and the constructing expression hosts are provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-2000
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(UNIL ) UNILEVER PLC.
(HIND-) HINDUSTAN LEVER LTD
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23-JUN-1999;
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pnvripfqviasdagllqapvqtsnlylavaeryeiiidftnfagqtldlrnv-aetndv
                                                                                                                                                                                                                                                                                                nadgtlrstegedqdlwgdvihvngqpwpflnvqprkyrfrflnaavsrawllylvrtss
                                                                                                                                                                                                                                                                                                                          TANGNLVTTNGELNSFWGDVIHVNGQPWPFKNVEPRKYRFRFLDAAVSRSFGLYFADTDA
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                                                 TINGVAFADVQNRLLANVPVGTVERWELINAGNGWTHPIHIHLVDFKVISRTSGNNARTV
                                                                                                                            GTDTDYDNTDKVMRFVVADDTTQPDTSVVPANLRDVPFPSPTTNTP--RQFRFGRTGPTW | : : | | : | : | : | : | : | : ; ;
                                                                                                                                                                                                                                                    IDTRLPFKVIASDSGLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNLGGSIGGI 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMSPGPTFQVPRGVETVVRFINNAEAPNSVHLHGSFSRAAFDGWAEDITEPGSFKDYYYP 161
                                                                                                gdedeyartlevmrfvvssgtve-dnsqvpstlrdvpfp-phkegpadkhfkfersnghy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594 AA;
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Pred. No. 3.1e-148;
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RESULT 1
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AC AAY9676
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the sequence of Stachybotrys chartarum phenol oxidizing enzyme. Phenol oxidizing enzymes encoded by nucleic acid sequences which hybridize to the coding DNA are claimed, as long as the enzyme is capable of modifying the colour associated with dyes or coloured compounds. The enzymes are useful in detergent compositions and for modifying colors associated with dyes or colored compounds which occur in stains in a sample. The enzymes are also useful for pulp and paper bleaching, anti-dye transfer in detergent and other textile applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New phenol oxidizing enzyme for modifying colors associated with or colored compounds, is obtained from fungus and is encoded by a nucleic acid comprising a specific nucleotide sequence
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23-JUN-1999;
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                                                                                    GMSPGPTFQVPRGVETVVRFINNAEAPNSVHLHGSFSRAAFDGWAEDITEPGSFKDYYYP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNATVFVDPMEELWQARPYELGEFQAQSGQFSVQAVTERIQTMAEYRPYAAADE 572
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                                                      gmspgptfnvprgtetvvrfinnatvensvhlhgspsrapfdgwaedvtfpgeykdyyfp
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                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     594 AA;
                                                                                                                                                                                                                                                                                           Conservative
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99US-0338723
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                                                                                                                                                                                                         56.2%; Score 1724.5; DB 21; 60.3%; Pred. No. 3.1e-148; tive 75; Mismatches 128; J
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M. carbonacea everninomicin biosynthetic pathway resistance gene product is useful for selecting for a transfected or transformed host cell. An integrative version of the vector is useful for introducing a everninomicin pathway gene (a bottle-neck gene) into an actinomycete of the genus Micromonospora. The DNA encoding the biosynthetic proteins is useful for synthesising novel everninomicin-related compounds, arising
                                                                                                                                                                       The sequence represents a Tailoring gene product, an oxidase, evrg. The protein comprises one of 98 enzymes of the everninomicin antibiotic biosynthetic pathway. A vector comprising
                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules encoding everninomicin pathway gene products, useful for improving yields of everninomicin, to proeverninomicin and as probes to identify homologous sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Everninomicin; antibiotic; bottle-neck gene; orthomicin;
fermentation; Tailoring gene product; oxidase;
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                                                                                                                                                                                                                                                                                              Claim 19;
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Corynebacterium

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from modifications of the DNA sequence designed to change glycosyl and modified orsellinic acid groups contained in everninomicin, for expressing functional or mutant everninomicin biosynthetic enzyme for evaluation, diagnosis and preferably biosynthesis of everninomicin or other secondary metabolic products, improving the yield of everninomicins and to produce novel everninomicins and also as a hybridisation probe to identify homologous sequences. The encoded polypeptides are useful for combinatorial biosynthesis to generate libraries of orthomycins, e.g. everninomicin analogues/homologues and drug discovery. The DNA encoding the integrates allows for increasing a given gene dosage. The integrative vector can be used to permanently integrate copies of a heterologous gene of choice into chromosomes of different hosts and to integrate genes which increase the yield of known products or to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel products such as hybrid antibiotics or other novel secondary metabolites. The vector can also be used to integrate antibiotic resistance genes in order to carry out bioconversions with compounds to which the strain is normally sensitive and is thus useful in fermentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                          ETVVVEAHYA-PFPGVYMFHCHNLIHEDHDMMA
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gsvkiqvtfatpylgqyvyhchylehsslgmma
                                                                                                                          VGTVERWELINAGNG----WTHPIHIHLVDFKVISRTSGNNARTVMPYESGLKDVVWLGRR
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polyketide or enzyme. The amino acids produced can be lysine, glutamine, glutamate, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleune, arginine, proline, histidine, tyrosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (I) or HA proteins encoded by then are used for diagnosing the presence or activity of Corynebacterium
                                                                                                                                                                                                                                                                                        proteinogenic or nonproteinogenic amino acid (preferred), purine or pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor,
                                                                                                                                                                                                                                                                                                                                                                            AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeos and adaptation (HA) proteins given in AAB79023 to AAB79242. The C. glutamicum HA genes (I) can be used in vectors for expression cells and production of fine chemicals, such as, an organic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 373-374; 712pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins
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                                                                                          used for diad
diphtheriae.
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theriae. (I) can be used to map the C. glutamicum genome or can as markers for genetically engineered Corynebacterium or habacterium. The HA proteins encoded by the (I) are used to maint ostasis in C. glutamicum or help the microorganism to adapt to.
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ALIGNMENTS

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Bilirubin oxidase precursor (EC 1.3.3.5). BWYTOTHECIUM VETRUCATIA. BUKATYOTA; FUNGI; ASCOMYCOTA; MITOSOPTIC ASCOMY NCBL_TAXID=5532; [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN=MT-1; MEDILINE=93366794; PubMed=8360171; KOİKEdA S., ANDO K., KAJİ H., INOUE T., MUTAO S. SAMEJİMA T.; MEDILINE=93366794; PubMed=8360171; KOİKEDA S., ANDO K., KAJİ H., INOUE T., MUTAO S. SAMEJİMA T.; MEDILINE=93366794; PubMed=8360171; KOİKEDA S., ANDO K., KAJİ H., INOUE T., MUTAO S. SAMEJİMA T.; MEDILINE=93366794; PubMed=8360171; KOİKEDA S., ANDO K., KAJİ H., INOUE T., MUTAO S. VETRUCATIA AND OTHER T., MUTAO OTHER T., MUTAO S. NOLECULE. -I. FUNCTION: OXIDATION OF BILIRUBIN AND OTHER T., COPACTOR; THIS PROTEIN BELONGS TO THE MULTIC CONTAIN THREE DISTINCT CU CENTERS KNOWN AS OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR. ATOMS PER MOLECULE. -I. SIMILARITY: BELONGS TO THE FAMILY OF MULTIC C. SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DO T. SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DO T. SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DO T. SIMILARITY: There a use by non-profit institutions as long as inmodified and this statement is not removed. Use the European Bioinformatics institutions as long as inmodified and this statement is not removed. Use the por send an email to licensee agreement (See http or send an email to licensee agreement (See http or send an email to licensee agreement (See http or send an email to licensee agreement (See http or send an email to licensee (SPE) SID. OXIDASE. DOMAIN 98 194 PLASTOCYANIN-LIKE DOMAIN 98 194 PLASTOCYANIN-LIKE DOMAIN 98 194 PLASTOCYANIN-LIKE DOMAIN 98 194 PLASTOCYANIN-LIKE DOMAIN 98 194 PLASTOCYANIN-LIKE DOMAIN 132 COPPER (TYPE 3) (B METAL 134 134 COPPER (TYPE 3) (B METAL 149 491 491 COPPER (TYPE 3) (B METAL 439 439 COPPER (TYPE 3) (B METAL 439 439 COPPER (TYPE 3) (B METAL 441 441 COPPER (TYPE 3) (B METAL 441 441 COPPER (TYPE 3) (B METAL 441 441 COPPER (TYPE 3) (B METAL 441 441 COPPER (TYPE 3) (B METAL 441 441 COPPER (TYPE 3) (B METAL 441 441 COPPER (TYPE 3) (B METAL 441 441 C	RESULT 1 BLRO_MYRVE ID BLRO_MYRVE AC Q12737; AC Q12737; DT 01-NOV-1997 DT 01-NOV-1997
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rubin oxidase precursor (EC 1.3.3.5). thecium verrucaria. tryocta; Fungi; Ascomycota; mitosporic Ascomycota; tryocta; From N.A., AND PARTIAL SEQUENCE. IN=My-1; leda S., Ando K., Kaji H., Inoue T., Murao S., Tak jima T.; ecular cloning of the gene for bilirubin oxidase ucaria and its expression in yeast."; function: Oxidation of bilirubin + (0/2) = biliverial COPACTOR: THIS POTEIN BELLONGS TO THE MULTICOPPER CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR. CONTA ATOMS PER MOLECULE. SIMILARITY: BELLONGS TO THE FAMILY OF MULTICOPPER SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS. SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS. SIMISS-PROT entry is copyright. It is produced th even the Swiss Institute of Bioinformatics and t european Bioinformatics Institute. There are no by non-profit institutions as long as its con fied and this statement is not removed. Usage b ties requires a license@isb-sib.ch). 1012579; BAA03166.1; 1014081; BAA03166.1; 101579; BAA03123.1; 11014081; BAA03166.1; 111579; BAA03123.1; 11198 BAA03123.1; 11199 BAA03123.1; 11199 BAA03123.1; 11199 BAA03123.1; 11199 BAA03123.1; 11199 BAA03169.1; Oxidoreductase; Glycop AL 132 Copper (TYPE 3) (BY SIMI LL 134 134 COPPER (TYPE 3) (BY SIMI LL 134 134 COPPER (TYPE 3) (BY SIMI LL 134 134 COPPER (TYPE 3) (BY SIMI LL 134 134 COPPER (TYPE 3) (BY SIMI LL 134 134 COPPER (TYPE 3) (BY SIMI LL 134 134 COPPER (TYPE 3) (BY SIMI LL 435 495 COPPER (TYPE 3) (BY SIMI LL 436 436 COPPER (TYPE 3) (BY SIMI LL 436 436 COPPER (TYPE 3) (BY SIMI LL 437 COPPER (TYPE 3) (BY SIMI LL 438 494 494 COPPER (TYPE 1) (BY SIMI LL 439 494 494 COPPER (TYPE 1) (BY SIMI LL 439 495 495 COPPER (TYPE 1) (BY SIMI COPPER (TYPE 3) (BY SIMI COPPER (TYPE 3) (BY SIMI COPPER (TYPE 3) (BY SIMI COPPER (TYPE 3) (BY SIMI COPPER (TYPE 3) (BY SIMI COPPER (TYPE 3) (BY SIMI COPPER (TYPE 3) (BY SIMI COPPER (TYPE 3) (BY SIMI COPPER (TYPE 3) (BY SIMI COPPER (TYPE 3) (BY SIMI COPPER	STANDARD;
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COPPER (TYPE 1) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Pred. No. 4.3e-214;
Mismatches 0;
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EMBL; AB007638; BAAZ2774.1; ALT_INIT.
EMBL; Z99107; CAB12449.1; -.
EMBL; X05578; CAA29165.1; ALT_INIT.
EMBL; X07512; CAA30392.1; -.
EMBL; U31756; AAC44642.1; -.
PIR; A27393; A27393.
SubtiList; BG10490; cott.
InterPro; IPR001117; Cu-oxidase.
Pfam; PF00394; Cu-oxidase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-88286730: PubMed=3135411;
Sandman K., Kroos L., Cutting S.M.,
"Identification of the promoter for
Bacillus subtilis and studies on the
late stage of sporulation.";
J. Mol. Biol. 200:461-473(1988).
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Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadaie Y.;
Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadaie Y.;
"Sequence analysis of the groESL-ootA region of the Bacillus subtilis
genome, containing the restriction/modification system genes.";
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STRAIN=168 / MARBI
MEDLINE=98116660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN BROWN PIGMENTATION DURING SPOROGENESIS.
-!- SIMILARITY: TO S.ANTIBIOTICUS PHENOXAZINONE SYNTHASE (PHSA).
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Donovan W., Zheng L., Sandman K., Losic)
"Genes encoding spore coat polypeptides
J. Mol. Biol. 196:1-10(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sporulation; CONFLICT
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Pred. No. 3.5e
77; Mismatches
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PTRGTHP -> RHAEHIL (IN REF. 1).
GPAVPPPP -> VRCPAAA (IN REF. 1).
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RESULT 3
PHSA_STRAT
                                                                                            Phenoxazinone synthase from Streptomyces antibiotics: purification of the large and small enzyme forms.";
Arch. Biochem. Biophys. 211:55-65(1981).

-i. FUNCTION: CATALYZES THE LAST BUT TWO STEPS IN THE PUTATIVE BIOSYNTHETIC PATHWAY OF ACTINOMYCIN.

-i. CATALYZES THE LAST BUT TWO STEPS IN THE PUTATIVE BIOSYNTHETIC ACTIVITY: 4 4-methyl-3-hydroxyanthraniloyl pentapeptide + 3 O(2) - 2 actinomycinic acid + 6 H(2)O.

-i. COPACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

-i. SUBUNIT: HOMODIMER (SMALL FORM) OR HOMOHEXAMER (LARGE FORM).

-i. SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

-i. SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q53692;
01-NOV-1997
01-NOV-1997
30-MAY-2000
              use by modified
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J. Bacteriol. 177:5740-5747(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHSA
                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
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STRAIN=IMRU 3720;
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(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
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STRAIRS / EMG2;
MEDLINE=97443975; PubMed=9298646;
MEDLINE=97443975; PubMed=9298646;
And Church G.M.;
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STRAIN+K12 / MG1655;
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01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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SUBCELLULAR LOCATION: Periplasmic (Potential).
SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete genome sequence of Escherichia coli K-12.";
nce 277:1453-1474(1997).
                                                     AE000121; AAC73234.1;
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                            EG12318;
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an email to license@isb-sib.ch).
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STRAIN=K12 / EMG2;
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Periplasmic; Signal;
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                       KSLPIPNHYGVDDFPVIIQDKRLDNFGTPEYNEPGSGGFVGDTLLVNGVQSPYVEVSRGW 228
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                                                                                                                                                                                                                                                                                                  SPECIES=S.typhi; STRAIN=CT18;

MEDLINE=21534947; PubMed=11677608;

Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagels K. Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Whitehead S. Barrar G., Simmonds M., Skelton J., Stevens K., Whitehead S. Barrar G., Shimmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                           Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Payan E., Sun H., Florea L., Miller W., Stoneking T., Nha
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SUFI OR STM3172 OR STY3349.
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Salmonella enterica serovar Typhimurium
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                                                       SUBCELLULAR LOCATION: Periplasmic (By Sim SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE CAUTION: Ref.1 sequence differs from that
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SEQUENCE
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LAC1_TRAVI
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                         Aphyllophorales; Coriolaceae; NCBI_TaxID=47662;
                                                                            Trametes villosa (White-rot fungus).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
                                                                                                                                          LCC1.
                                                                                                                                                                                             Laccase
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InterPro; IPR001117; Cu-oxidase.
Pfam; PF00394; Cu-oxidase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLPIPPVKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLGSADLVGYDGMSPGPTFQV 111
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                                                                                                                                                           97 (Rel. 35, Created)
97 (Rel. 35, Last sequence update)
97 (Rel. 35, Last annotation update)
97 (Rel. 35, Last annotation update)
precursor (EC 1.10.3.2) (Benzenedio oxidase) (Diphenol oxidase).
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1 27 BY SIMILARITY.
28 470 PROTEIN SUFI.
68 164 PLASTCCYANIN-LIKE.
70 AA; 51858 MW; 61E84D4D42B025FB
                                                                                                                                                                                                                                                                                                                                   STANDARD
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IPPVKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLGSADLVGYDGMSPGPTFQVPRG

VSPDGFSRQAVVVNGGTPGPLITGNMG

62

APNSVHLHGSFSRAAFDGWAE---

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Query Match
Best Local Similarity
Matches 126; Conser

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70;

Score 228.5; Pred. No. 3.5e 70; Mismatches

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InterPro; IPR003155; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yaver D.S., Xu F., Golightly E.J., Brown K.M., Brown S.H., Rey M.W., Schneider P., Halkier T., Mondorf K., Dalboge H.; "Purification, characterization, molecular cloning, and expression two laccase genes from the white rot basidiomycete Trametes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES
-!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone
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COPACTOR: BINDS 4 CU-IONS PER MOLECULE. THR COENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
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SUBCELLULAR LOCATION: Secreted.
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361
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455
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MULTICOPPER_OXIDASE2; FALSE_NEG
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302
491
85
87
130
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Multigene family.
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PLASTOCYANIN-LIKE
PLASTOCYANIN-LIKE
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MEDLING-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein suff homolog precursor.
SUFI OR HI0733.
                                                                                                                                                                                                     Science 269:496.512(1995).
-!- SUBCELLULAR LOCATION: Periplasmic (Potential).
-!- SIMILARITY: STRONG, TO E.COLI AND S.TYPHIMURIUM
-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
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                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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Best Local 9
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01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, L
15-JUL-1998 (Rel. 36, L
Laccase precursor (EC 1
                                                                                                                                                                                                                                                                                                               LAC-1
                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=92314427; PubMed=1535523;
                                                                                                                                                                                                                                                             Eukaryota; Fu
Diaporthales;
                                                                                                                                                                                                                                                                                                                                                                                                                     CRYPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Periplasmic; Signal; SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32756; AAC22390.1; TIGR; HI0733; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                         -i- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION PRODUCTS (PROBABLE).
-i- CATALYTIC ACTIVITY: 4 benzenediol + O(2) =
                                                                                                                                                hypovirulent strain.";
Mol. Plant Microbe Interact.
                                                                                                                                                                                   Choi G.H., Larson T.G., Nuss D.L.; "Molecular analysis of the laccase
                                                                                                                                                                                                                                                                                                  Cryphonectria parasitica (Chesnut blight fungus) (Endothia
                                                                                                                                                                                                                                                                                                                                                                                                       LAC1_CRYPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                        parasitica)
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                  SUBCELLULAR LOCATION: Secreted (Potential).
SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES
SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                         H(2)O.
COFACTOR: BINDS 4 CU-IONS PER MOLECULE.
CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2
3 OR COUPLED BINUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVPLPIPPVKQPRLTVTNPV---NGQEIWYYEVEIKPFTHQVYPDLGSADLV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVPAPLLAASREKLVVPPLIEVRRGRPI-----VLTMQETNYPLDGSHNVTVWGFNGNY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DQEMLLIAQDLGFLPKAKSVKSLVLSPGERAEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLQLFKQNQPH-FYGNRLLVNGIEAPYLDVARGWIRLRLLNASLARAYDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGPTFQVPRGVETVVRFINNAEAPNSVHLHGSFSRAAFDGWAEDITEPGSFKDYYYPNRQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLPFKVIASDSGLLEHPADTSLLYISMAERYEVV
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es; Valsaceae;
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311
164
34496 h
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25.9%;
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BY SIMILARITY
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Last annotation update)
1.10.3.2) (Benzenediol:oxygen oxidoreductase)
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PLASTOCYANIN-LIKE.
MW; 436173F59F1E1772 CRC64;
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TION AND DETOXIFICATION OF LIGNIN-DERIVED
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Pred. No. 1
                                                                                                                                                                                                                                                                          Pezizomycotina;
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EMBL; S38903;
HSSP; P37064;
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InterPro; IPR002355; MultiCu_oxidse2.
                                                             271
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328 TIELRNLGGSIGGIGTDTDYDNTDKVMRFVVADDTTQPDTSVVPA--
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                                                          SFGLYFADTDAIDTRLPFKVIASDSGLLEHPAD---TSLLYISMAERYEVVFDFSDYAGK
                                                                                         LVVYTQSNAPPASDNVLFNG-----TNINPANTTQGQYKTITLTPGKRHRLRIINTSVEN
                                                                                                                                                      WYHS---HFSAQYG-NGIVGAIQIDGPA----SLP-----YDIDLGPLVLSDYYYKTADE
                                                                                                                                                                                   WYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDI - - - PMILTSKQYTANGN
                                                                                                                                                                                                                  SYTYTNNLKYNGTTIHWHGIRQLNTNLQDG-VNGITECPIPPNGGSKTYTFIAHQYG-TS
                                                                                                                                                                                                                                               VVRFINNAE-APNSVHLHG--SFSRAAFDGWAEDITE----PGSFKDYYYPNRQSARTL 169
                                                                                                                                                                                                                                                                             ROYDLTLTQAEN----W-----LGPDGVVKEDVMLVNGNILGPVIHAQWGDTI 110
                                                                                                                                                                                                                                                                                                           KOPRLIVTNPVNGOEIWYYEVEIKPFTHQVYPD-LGSADLVGYDGMSPGPTFQVPRGVET 117
                                                                                                                                                                                                                                                                                                                                                                         AALSLLFNSNAVQASP-----VPETSPATGHLFKRVAQISPQYPMFT----VPLPIP-PV
                              NEQUSIVGHS---
                                                                                                                    LYTTNGELNSFWGDVIHVNGQPWPFKNVEP-----
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138; Conser
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                             -MTVIESDF----VPVDSFTTDSLFVGIGQRYDVTIDASQATDN
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Pred. No. 9.
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AC Q12719;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase 4 precursor (EC 1.10.3.2) (Benzenediol:oxygen
CUrishol oxidase) (Diphenol oxidase).
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
                                                                                                         PROSITE; PS00079; MULTICOPPER_OXIDASE1; PROSITE; PS00080; MULTICOPPER_OXIDASE2; Oxidoreductase; Signal; Copper; Metal-bi
                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: LIGNIN DEGRADATION AND DETÓXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE).
-i- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95399443; PubMed=7669813;
Joensson L.J., Sjoestroem K., Haeggstroem I., Nyman P.C
"Characterization of a laccase gene from the white-rot
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                                                                                                                                                                   InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
                                                                                                                                                                                                              EMBL; X84683;
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SEQUENCE FROM N.A.

MEDLINE-97128774; PubMed-8973314;
Yaver D.S., Golightly E.J.;
"Cloning and characterization of the white-rot basidiomycete Trametes vilaccase gene family.";
Gene 181:95-102(1996).
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InterPro; IPR002355; MultiCu_oxidse2
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Trametes villosa (White-rot fungus).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Aphvllophorales; Coriolaceae; Trametes.
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PRODUCTS (PROBABLE).
-!- CATALYTIC ACTIVITY: 4 benzenediol +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase;
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NCBI_TaxID=47662;
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Laccase 4 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H(2)O.
COPACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CONTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
SUBGULIT: HOMODIMER (BY SIMILARITY).
SUBGELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degradation;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Laccase 5 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Diphenol oxidase) (Laccase IV).
LCC5 OR LCCIV.
                                                                                                                                                                               Trametės versicolor (White-rot fungus).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Aphyllophorales; Coriolaceae; Trametes.
                                                                                 "Cloning and sequence analysis of two latter lighthough the lighthough the basidiomycete Trametes Gene 196:113-119(1997).
                                                                                                                   ong
                                                                                                                              MEDLI
                                                                                                                                                                     Aphyllophorales;
NCBI_TaxID=5325;
                                                                                                                                                 SEQUENCE FROM N.A.
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H(2)O.

COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DIST:
CCENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL,
3 OR COUPLED BINUCLEAR (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted.
                                                   FUNCTION: LIGNIN DEGRADATION AND I PRODUCTS (PROBABLE).
CATALYTIC ACTIVITY: 4 benzenediol
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                                                                                                                 INE=97464057; PubMed=9322748; E., Pollock W.B., Smith M.;
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ-i- FUNCTION: LIGNIN DEGRADATION AND DETOXIFIC PRODUCTS (PROBABLE).

-i- CATALYTIC ACTIVITY: 4 benzenediol + O(2) =
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InterPro; IPR002355; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
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Aphyllophorales; (
NCBI_TaxID=47662;
                                                                                                      EMBL; L78078; AAB47735.2; HSSP; P37064; 1AOZ.
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MEDLINE=97128774; PubMed=8973314;
Yaver D.S., Golightly E.J.;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laccase 5 precursor (EC 1.10.3.2) (Benzenedio (Urishiol oxidase).
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SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES
SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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COFACTOR: BINDS
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R EMBL; M60561; AAA33104.1; -.

R PIR; A35883; A35883; Cu-oxidase.

R InterPro; IPR0031117; Cu-oxidase.

R InterPro; IPR002355; MultiCu_oxidse2.

Pfam; PF00394; Cu-oxidase; 3.

DR Pfam; PF00394; Cu-oxidase; 3.

DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.

DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.

DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kojima Y., Tsukuda Y
Sakaino M., Kita Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
STRAIN=IFO 4917;
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol.oxygen
(Urishhol oxidase) (Ligninolytic phenoloxidase).
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Q02497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning, sequence analysis, and expression of ligninolytic phenoloxidase genes of the white-rot basidiomycete Coriolus
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FUNCTION: MOST PROBABLY PLAYS AN IMPORTANT DEGRADATION. CLEAVES THE C-C AND C-O BONDS MODEL COMPOUNDS (SUCH AS O- AND P-QUINOLS,
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3 OR COUPLED BINUCLEAR.
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Coriolaceae; Coriolus.
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Eukaryota; Fungi; Aphyllophorales; (NCBI_TaxID=5325; [1]

Trametes versicolor

Fungi;

Basidiomycota;

(White-rot

fungus).

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Hymenomycetes;

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Matches 121
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Ong E., Pollock W.B., Smith M.;
"Cloning and sequence analysis of two laccase complementary DNAs from the ligninolytic basidiomycete Trametes versicolor.";
Gene 196:113-119(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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InterPro; IPR002355; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
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EMBL; U44430; AAC4
HSSP; P37064; 1AOZ
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3 OR COUPLED BINUCLEAR (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted.
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FHCHNLIHEDHDMMAAFNATVLPDYGYNATVFVDPMEELWQARP 536	PIHIHLVDFKVISRTSGNNARTVMPYESGL-KDVVWLGRRETVVVEAHYAPFPGVYM 492 	TWTINGVAFADVQNRLLANVPVGTVERWELINAGNGWTH 436	DKVMREVVADDITQPDTSVVPANLEDVP-FPSPTTNTPRQFREGRTGP 397	SGLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNLGGSIGGIGTDTDYDNT 350	NGQPWPFKNVE-PRKYRFRFLDAAVSRSFGLYFADIDAIDTRLPFKVIASD 294	LYMLTDPAEDALNLPSGYGEFDIPMILTSKQYTANGNLVTTNGELNSFWGDVIHV 244 ::: :	139 RAAFDGWAEDITEPGSF-KDYYYPNRQSARTLWYHDHAMHITAENAYRGQAG 189

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0XIDOREDUCTASE-LIKE PROTEIN.
                                                                                                                                                                                                                                                    Kormanec J., Bistakova J., Novakova R., Homerova D., Re "Cloning and characterization of a new polyketide gene streptomyces aureofaciens CCM3239."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL, AY033994; AAK61713.1;
                                                                                                                                                                                                                                                                                                                                                                               Streptomyces aureofaciens.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Str
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Federspiel N.A., Palm C.J., Conway A.B., Kurtz D. Federspiel N.A., Palm C.J., Conway A.B., Kurtz D. Au M., Araujo R., Buehler E., Dewar K., Feng J., Oji O., Osborne B.I., Shinn P., Sun H., Toriumi I Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (Apr.1997) to the EmBL/GenBank/DDBJ da:
EMBL; AF000657; AAB72167.1;
InterPro; IPR001117; Cu-oxidase; 1.
Pfam; PPF00394; Cu-oxidase; 1.
SEQUENCE 568 AA; 64355 MW; C4314C889576E35E
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023123;
01-JAN-1998
01-JAN-1998
01-DEC-2001
F19G10.5 PRO:
F19G10.5.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; edicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                             LHGSFSRAAFDGWAEDITEPGSFKD-
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                                                                                                                                    GYDGMS------PGPTFQVPRGVETVVRFIN-------NAEAPNSVH 132
                                                                                                                                                               MFVDDLP----DMPRLYGFNSVHG-----IIKPASLQIGMFSTKWKFHRDLPATPVF
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LAGLVGAYILRHHAVESPFQLPTG-DEFDRPLIIFDRSFRKDGSIYMNATGNNPSIHPQW
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P., Sun H., Toriumi M., Vyc.
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01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone:P0409B08.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AP002B60; BAB18287.1;
InterPro; IPR002355; MultiCu_oxidse2.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE SPORE COAT PROTEIN-LIKE PROTEIN.
P0409B08.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coat protein SEQUENCE 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9FTS3
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hes 174;
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                                                                                                                                                                                                                                                                           PVNG--QEIWYYEVEIKPFTHQVYPDLGSADLVGYDGMS------PGPTFQVPRGVETTV 119
                                                                                                                                                                                                                                                                                                                                                                                                       PVPETSPATG ------HLFK-----RVAQISPQYPMFTVPLPIPPVKQPRLTVTN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YA-----PF----PGVYMFHCHNLIHEDHDMM 506
TWTRKTYTYPNVQAPGNLWYHDHALGLTRVSLLAGLLAAYVIEKPELEDPMNLPC--GDH
                                                   F---KDYYYPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDP-AEDALNLPSGXGEE
                                                                                                                                                                                                                                                                                                                                        PLP--APAAGRRRWPVMTSLNLTKYVDSLPRIAKIRGYGIRHGRPVPI-----KLTZ-- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFADVQNRLLAN-----VPV-----GTVERWELINAGNGWTHPIHIHLVDFKVISRTS- 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSAYLSKPVMTKSILLSPSEIVDVVVDFYKSPSRTVVLAN-----DAPYPYPSGD
                                                                                                         EWQNHLPDAHILPWDPKVPTAIPKKGGVPTVVHLHGGAHPPEEDGHAFAWFTRDFAENGS
                                                                                                                                                                                                                              ---GMYSKTWQFHRDMPPTPVFVY-------GQSLQTATFPGPTIVARQGVP5jaV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YIHTNASYPFDPTQEPG-YVYHCHILDHEDNMMM 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           637 AA; 70919 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.48;
                                                                                                         ; Score 502; DB 10;
; Pred. No. 2.6e-29;
72; Mismatches 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              692D39F10F2D6A96 CRC64;
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                                                                                                       Query Match
Best Local s
Matches 175
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Q9AWU4;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                          Sasaki T., Matsumoto T., Yamamoto K.;

"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,

clone:P0037004.";

submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AP002909; BAB21188.1;

EMBL; AP002333 BAB5544.1;

InterPro; IPR002355; Multicu_oxidse2.

PROSITE: PS00809; MULTICOPPER_OXIDASE2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                             "Oryza sativa nipponbare(GA3) genomic DNA, clone:P0044F08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. NCBI_TaxID=4530;
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                       STRAIN=CV.
                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. NIPPONBARE
Sasaki T., Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUTATIVE SPORE COAT PROTEIN. P0044F08.18 OR P0037C04.31.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I-----RLTI-----GMYQKKWKFHRDLPASTVFVFGTSAAT-----ATFPGPTIEAA 110
                                                                           AALSLLFNSNAVQASPVPETSPATGHLFKRVA-----QISPQYPM---FTV----PLP
                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INL-TGDNHPLHLHIATFQAIKMTKIEGFQVFKDCMIKNNNTATCNLDQHAVGPVVPVPE
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                         IPPVKQPRLTVTNPVNG--QEIWYYEVEIKPFTHQVYPDLGSADLVGYDGMSPGPTFQVP 112
                                                   AVLLLVLVGVAAGTRPPSAPPPVTEDTLQKVAGSLEMYVDELPQMPKIYGFSMRHGHPSP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEKTWKNAVKIPPEFMTSVVVAFRLVEANQPYPFDATTEPG-FVYHCHILDHEDNAMI
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                                                                                                        al Similarity
175; Conserv
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                                                                                                                                                                                                                                                                                                          NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                       NIPPONBARE;
                                                                                                                                                                        582 AA;
                                                                                                       Conservative
                                                                                                                                                                        64050 MW;
                                                                                                                16.1%; 29.2%;
                                                                                                                                                                                                                                                                                                                                                                                         ., Yamamoto K.;
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                                                                                                     73;
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Last annotation update)
                                                                                                     Score 495; DB
Pred. No. 7.6e
73; Mismatches
                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                   DB 10;
.6e-29;
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                                                                                                                                                                                                                                                                                                                                                  databases
                                                                                                                              Length 582;
                                                                                                        Indels 132;
                                                                                                     Gaps
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Q949X9;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                  Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R. W., Ecker J.R., Theologis A., "Full Length cDNA of gene F23N2O.3 (GI:12323429)."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                 EMBL; AY050818; AAK92753.1; Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyla; edons; core eudicots; Rosid.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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84
                                                       91 DLGSADLVGYDGMS-----PGPTFQVPRGVETVVRFIN----
                                                                                                                                           Local
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581 AA;
DLPATPVFAY-GTSKRSATVPGPTIEAVYGVDTYVTWRNHLPLHHILPWDPTISPAIPKH 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VINLTPD-NHPLHLHLATFQATRVRGLVDEDAFKGCMAKLNDAVRCNVSRHAVGEEVAVP
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156; Conserv
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Last annotation update)
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                                                                                                            Score 485; DB 10;
Pred. No. 4.2e-28;
6; Mismatches 183
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                                                                                                    RX MEDLINE=21016719; PubMed=11130712;
RY Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA Theologis A., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Chan C., Chen H., Cheuk R.F., Chin C.W.,
RA Duehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Condsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Milltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Miltscher J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sakano H., Tallon L.J., Tambunga G., Toriuumi M.J., Town C.D.,
William M., Walker M., Walker M.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09C9A4 PRELIMINARY; PRT; 591 AA. 09C9A4; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence up 01-JUN-2001 (TrEMBLrel. 17, Last annotation SPORE COAT PROTEIN-LIKE PROTEIN. E23N20.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                       Nature 408:816-820(2000).
EMBL; AC016972; AAG51692.1;
                                                                                      thaliana.";
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AA;
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67358
MW;
BOCE7BBOE8F05AAF
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     Query Match
Best Local Similarity
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                                                                          PROSITE; PSOC
Coat protein.
SEQUENCE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FTS5;
Q9FTS5;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 16, Last sequence update)
PUTATIVE SPORE COAT PROTEIN-LIKE PROTEIN.
P0409B08.12.
                                                                                                        Submitted (AUG-2000) to the EMBL/GenBank/DDBJ data EMBL; AP002860; BAB18285.1; -. InterPro; IPR002355; MultiCu_oxidse2.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1.
                                                                                                                                                                         STRAIN-CV. NIPPONBARE;
Sasaki 7. Matsumoto 7., Yamam
"Oryza sativa nipponbare(GA3)
clone:P0409B08.";
                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLPATPVFAY-GTSKRSATVPGPTIEAVYGVDTYVTWRNHLPLHHILPWDPTISPAIPKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WT-INGVAFADVQNRLLANVP-VGTVE-----RWELINAGNGWTHPIHIHLVDFK 446
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                                                                                                                                                                                                                                                                                                                                                   sativa (Rice).
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                                                                        68321 MW;
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27
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       . 48;
                                                                                                                                                                                                              Yamamoto
        Score
Pred.
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Pred. No. 5
                                                                                                                                                                                         moto K.;
genomic DNA,
                                                                          80C6EC856E305193 CRC64;
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       456;
No.
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       6.9e-26;
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.8e-27;
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                        614;
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 SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBA
Sasaki T., Matsumot
"Oryza sativa nippo
                                                                                                                                                                                                                         Oryza sativa (Rice).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnollophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                      STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamam
"Oryza sativa nipponbare(GA3)
clone:P0409B08.";
                                                                                          Submitted
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                           NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      596
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NIPPONBARE;
Matsumoto T., Yamamoto
iva nipponbare(GA3) geno
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Matches
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O9FTS6;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation updat-
putative spore coar protein-Like protein.

p0409B08.11 OR p0044F08.29.
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                                                                                                        EMBL/GenBank/DDBJ
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genomic DNA,
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                                                                            067206; PRELIMINARY; 067206; OT-AUG-1998 (Tremblrel 07, 01-AUG-1998 (Tremblrel 19, 01-DEC-2001 (Tremblrel 19, PERIPLASMIC CELL DIVISION P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002860; BAB18284.1; -. EMBL; AP002909; BAB21194.1; -. Interfro; IPR002355; MultiCu_oxidse2. PROSITE; PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1.
SEQUENCE
                         Bacteria; Aquificales; NCBI_TaxID=63363;
                                                   Aquifex aeolicus.
                                                                   SUFI OR AQ_1130.
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SEQUENCE 588 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFDFSDYAGKTIELRN-----LGGSIGGIGTDTDYDNTDKVMRFVVADD--TTQPDTS
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FROM N.A
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26.6%;
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07, Last sequence update)
19, Last annotation update)
ON PROTEIN (SUFI).
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Pred. No. 8.4e-26;
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InterPro; IPR002355; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2;
Cell division; Complete proteome.
SEQUENCE 527 AA; 59490 MW; F361BF79
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                                         Bacteria; I
Salmonella
                                                                       Salmonella typhimurium
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EMBL; AE000724; AAC07157.1;
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SEQUENCE FROM N.A.
                            NCBI_TaxID=602;
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"cuiD, a gene encoding a multicopper oxidase following and characterization.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AY053392; AAL15149.1;
SEQUENCE 536 AA; 58532 MW; DAE43663N1R17R7
                                                                                                                                                                                                                                                                                      Pasteurella murtocce.
Pasteurella murtocce.
                                                                     MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006230; AAK04022.1; -.
                                                                                                                                           MEDLINE-21145866; PubMed-11248100; May B.J., Zhang Q., Li L.L., Paust
                        InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2
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Pred. No. 9.1e
53; Mismatches
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                                                                                                                                                                                                                                                                                                          subdivision;
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. No. 9.1e-22;
ismatches 201;
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Pm70.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q98FW8;
01-OCT-2001
                         EMBL;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed=11214968;
                                                                                                              Kaneko T., Nakamira Y., Sato S., Asamizu E., Kato S., Kaneko T., Nakamira Y., Sato S., Asamizu E., Kato S., Kaneko T., Kaneko T., Kaneko T., Kaneko T., Kaneko T., Kaneko T., Kaneko T., Kaneko T., Kaneko T., Kaneko T., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2001
01-OCT-2001
                                                                     "Complete genome structure of Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                     Phyllobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti)
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                                                DNA Res.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=381;
     InterPro;
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AP003002; BAB50448.1; -.
Pro; IPR001117; Cu-oxidase
                                                   7:331-338(2000)
                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 18, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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58572 MW;
                                                                                                                                                                                                                                                                                                                                                                  teria; alpha subdivision; Mesorhizobium.
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Pred. No. 2.9e-21;
6; Mismatches 202;
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ima K., Kimura
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EMBL; AE006045; AAK02188.1; -.
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                                                                   Score 288; DB
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83; Mismatches
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                                                Submitted (APR-1999) to the EMBL/GenBank/DDBJ EMBL; Z25774; CAA81037.1; -. InterPro; IPR001865; Ribosomal_S2. PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 SEQUENCE
                                                                                                                       STRAIN-SS-
                                                                                                                                                                                                                                                                                  Corstjens
                                                                                                         Corstjens P.L.;
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                                                                                                                                  373 NLRDVPFPSPTT----NTPRQFRFGRTGPTWTINGVAFADVQNRLLANVPVGTVERWELI 428
                                                                                                                                                                                                                                                                       640 GLLPKVABIAPTPVGYQLDKGRITVLNVLTTGLYLGNAERADVLVDLSAYAGKTLIVYND 699
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804 PSLNG 808
                                            429 NAGNG 433
                                                                                          757 QIRDARQRGDSTALKAEIPKAYAIAQEKP-----VVGQDVYNQAL-----GTT--WGAT 803
                                                                                                                                                                                 700 SGAPVPAGDPRNDYFTAVGDQSDAGGAEDTKPGYGPNTRTMMQIKVRAAITTPS---FDG 756
                                                                                                                                                                                                                                    335 GGS-----IGGIGTDTDY-----DNTDKVMREVVADDTTQPDTSVVPA.372
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Search completed: October 3, 2002, 11:03:23 Job time: 462 sec

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Result
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ALIGNMENTS

; ORGANISM: Stachybotrys charatum US-09-401-476-4 FILE REFERENCE: GC584 CURRENT APPLICATION NUMBER: US/05 CURRENT FILING DATE: 1999-09-22 NUMBER OF SEQ ID NOS: 8 APPLICANT: Wang, Huaming TITLE OF INVENTION: No. 6168936el Phenol Oxidizing SEQ ID NOS: 8 FastSEQ for Windows Version 3.0 US/09401476 US/09/401,476

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ОY	181	ENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSKQYTANGNLVTTNGELNSFWGD 240	_
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Ωy	301	PADTSLLYISMAERYEVVFDFSDYAGKTIELRNLGGSIGGIGTDTDYDNTDKVMRFVVAD 360	_
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CURRENT APPLICATION NUMBER: US/09/401,476;
CURRENT FILING DATE: 1999-09-22;
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0;
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Pred. No. 1.1e-186;
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; MOLECULE TYPE:
US-09-032-315-2
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APPLICANT: Svends
APPLICANT: Xu, Fe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, CATO1
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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SOFTWARE: FastSE
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CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 27-FEB-1998
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YAGKTIELR----NLG--GSIGGIGTDTDYDNTDKVMRF----VVADDTTQPDTSVVPANLR
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Pred. No. 1.1e-13;
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                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                     TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: RESERVED TO STATE OF INVENTION: LACCASE MUTANTS
TITLE OF INVENTION: LACCASE MUTANTS
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115 VETVVRFINNAE-----APNSVHLHGSFSRAAFDGWAE-----
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                                                              55 IPPVKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLGSADLVGYDGMSPGPTFQVPRG 114
                                                                                                     Local Similarity
nes 126; Conserv
                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-80/-014
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: DE CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         LENGTH:
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                                 IGPVAD--LTITNAA-----------VSPDGFSRQAVVVNGGTPGPLITGNMG 41
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Schneider, Palle
Rasmussen, Grethe
                                                                                                     Conservative
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                                                                                                7.5%; Score 228.5; DB 2; 22.8%; Pred. No. 1.1e-13; tive 70; Mismatches 212;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993/31
FILING DATE: December 18, 199
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
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                                                                                                                                                                                                                                                                                                                                                                                              405 Lexington Avenue
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Schneider, Palle
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Der 18, 1997
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                                         5032.200-US
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US-09-396-260-2; Sequence 2, Application US/09396260; Patent No: 6184015
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                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                  APPLICANT: SVENUS...
APPLICANT: XU, Feng
APPLICANT: XU, Feng
TITLE OF INVENTION: LACC
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 618401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.5%; Score 228.5; DB 4; Best Local Similarity 22.8%; Pred. No. 1.1e-13; Matches 126; Conservative 70; Mismatches 212;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        GENERAL INFORMATION:
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COMPUTER READABLE FORM
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                                       COUNTRY:
                                                       CITY: New York
STATE: NY
                                                                                            ADDRESSEE: No. 61840150 No. 1
STREET: 405 Lexington Avenue
                      ZIP:
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                                                                                                                     6184015o No. 6184015disk of No. 6184015th America, Inc
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Best Local Similarity
Matches 126; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
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NAME: Rozek, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/032,315
FILING DATE: 27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
  474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 VETVVRFINNAE-----APNSVHLHGSFSRAAFDGWAE------DITEPGSF-KDYYY 160
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COMPUTER: IBM CON
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/396,260
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                                                                           NPIFRDVVSTGTPAAGDNVTIRFR-TDNPGPWFLHCHIDFHLEAGFAVVF-AEDIPD---
                                                                                                                                                                                                                                                                               DVPFPSPTTNTPR------QFRFGRTGPTWTINGVAFADVQNRLLANVPVGTVER 424
-- VASANPVPQAW
                                   NATVFVDPMEELW
                                                                                                                   SGL-KDVVWLG---RRETVVVVEAHYAPFPGVYMFHCHNLIHEDHDMMAAFNATVLPDYGY 519
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FastSEQ for Windows Version 2.0
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IBM Compatible
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                                                                                                                                                                                               ---GWTHPIHIHLVDFKVISRTSGNNARTVMPYE 463
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 50:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein -576-281-2
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APPLICATION NUMBER:
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324 YAGKTIELR---NLG--GSIGGIGTDTDYDNTDKVMRF---VVADDTTQPDTSVVPANLR 375
                                                                                                                                                                                                                                161 PNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSKØ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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                                                                                                                                                                                                                                                                                                                                                                                        55 IPPVKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLGSADLVGYDGMSPGPTFQVPRG 114
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TELEFAX: 212-878-9655
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                                                                                                                                                                                  PDQ--AGTFWYHSH-LSTQYCDGLRGPFVVYDPNDPAADLYDVDN-----DDTVITLVDW 251
                                      NYTESIDGHNMTIIETDSINTA-------PLVVDSIQIFAAQRYSEVLE-AN
                                                                                                                     YHVAAKL----GPAFPLGADATLINGKGRSPSTTTADLSVISVTPGKRYRFRLVSLSCDP 207
                                                                                                                                                                                                                                                                         DRFQLNVIDNLTNHTMLKSTSIHWHGFFQKGT--NWADGPAFINQCPISSGHSFLYDFQV 99
                                                                                                                                                                                                                                                                                                                                                      IGPVAD--LTITNAA--------VSPDGFSRQAVVVNGGTPGPLITGNMG 41
                                                                             SF-----GLYFADTDAIDTRLPFKVIASDSGLLEHPADTSLLYISMAERYEVVFDFSD 323
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Svendsen, Allan
Schneider, Palle
Rasmussen, Grethe
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US-08-462-484-2
; Sequence 2, Application US/08462484
; Patent No. 5667531
; MOLECULE TYPE:
; ORIGINAL SOURCE:
; ORGANISM: POL
US-08-462-484-2
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                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,147
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: APPLICANT:
                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
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MEDIUM TYPE: Floppy disk
                                                                                                                                                               SEQUENCE CHARACTERISTICS
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TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 05-JU
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CITY: New York
                                                                                 TOPOLOGY: lin
                                                                                                                                                                                                                                                                                       NAME: Lowney, Karen A REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                         LENGTH:
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Dalboge, Henrik
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Query Match Best Local Similarity

7.5%; 22.8%;

Score 228.5; DB 1 Pred. No. 1.2e-13;

DB 1;

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                                                                                                                                                                                                                                                                                                      APPLICANT: Dalboye,
APPLICANT: Dalboye,
APPLICANT: Schneider, Palle
APPLICANT: Aaslyng, Dorrit A.
APPLICANT: Aaslyng, DURIFIED POLYPORUS LACCASES
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,147
FILING DATE: 15-MAY-1995
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT
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                                                                                                                                                                                         STATE: New York COUNTRY: U.S.A. ZIP: 10174-6401
                   CLASSIFICATION:
                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGL-KDVVWLG---RRETVVVEAHYAPFPGVYMFHCHNLIHEDHDMMAAFNATVLPDYGY 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVPFPSPTTNTPR------QFRFGRTGPTWTINGVAFADVQNRLLANVPVGTVER 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAGKTIELR---NLG--GSIGGIGTDTDYDNTDKVMRF---VVADDTTQPDTSVVPANLK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATVFVDPMEELW 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPIFRDVVSTGTPAAGDNVTIRFR-TDNPGPWFLHCHIDFHLEAGFAVVF-AEDIPD--- 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDLLPSGSVYSLPSNADIEISFPATAAAPGAPHPFHLHGHAFAVV-RSAGS---TVYNYD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WELINAGN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHVAAKL----GPAFPLGADATLINGKGRSPSTTTADLSVISVTPGKRYRFRLVSLSCDP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTANGNLYTTNGELNSFWGDVIHVNGQ------PWPFKNVEP-RKYRFRFLDAAVSR 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SF-----GLYFADTDAIDTRLPFKVIASDSGLLEHPADTSLLYISMAERYEVVFDFSD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDQ--AGTFWYHSH-LSTQYCDGLRGPFVVYDPNDPAADLYDVDN-----DDTVITLVDW
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                                                                                                                                                                                                                                                                    No. 57704180 No. 5770418disk of No. 5770418th America, Inc. 5 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GWTHPIHIHLUDFKVISRTSGNNARTVMPYR 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VSPDGFSRQAVVVNGGTPGPLITGNMG
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PCT-US95-07536-2
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                                                                                                          Sequence 2, Application PC/TUS9507536 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                 APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
                                                                                           APPLICANT
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CORRESPONDENCE ADDRESS:
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mes 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 DRFQLNVIDNLTNHTMVKSTSIHWHGFFQKGT--NWADGPAFINQCPISSGHSFLYDFQV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lowney, Karen A REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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Best Local Similarity
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-June-199.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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TYPE: amino acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 IGPVAD--LTITNAA-------VSPDGFSRQAVVVNGGTPGPLITGNMG 62
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TELEFAX: 212 878 9655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
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                                                                           QDLLPSGSVYSLPSNADIEISEPATAAAPGAPHPFHLHGHAFAVV-RSAGS---TVYNYD
NPIFRDVVSTGTPAAGDNVTIRFR-TDNPGPWFLHCHIDFHLEAGFAVVF-AEDIPD---
                                                                                                                                                                                                 DVPFPSPTTNTPR------QFRFGRTGPTWTINGVAFADVQNRLLANVPVGTVER 424
                                                                                                                                                                                                                                                                               YAGKTIELR---NLG--GSIGGIGTDTDYDNTDKVMRF----VVADDTTQPDTSVVPANLR 375
                                                                                                                                                                                                                                                                                                                                                               SF-----GLYFADTDAIDTRLPFKVIASDSGLLEHPADTSLLYISMAERYEVVFDFSD 323
                                                                                                                                                                                                                                                                                                                                                                                                       YHVAAKL----GPAFPLGADATLINGKGRSPSTTTADLSVISVTPGKRYRFRLVSLSCDP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                               YTANGNLVTTNGELNSFWGDVIHVNGQ------PWPFKNVEP-RKYRFRFLDAAVSR 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSKQ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRFQLNVIDNLTNHTMVKSTSIHWHGFFQKGT--NWADGPAFINQCPISSGHSFLYDFQV 120
                                 SGL-KDVVWLG---RRETVVVEAHYAPFPGVYMFHCHNLIHEDHDMMAAFNATVLPDYGY 519
                                                                                                                     WELINAGN----
                                                                                                                                                         NL-HPLVTTAVPGSPVAGGVDLAINMAFNFNGTNFFINGTSFTPPTVPVLLQIISGAQNA 383
                                                                                                                                                                                                                                       QAVDNYWIRANPNFGNVGFTGGINS-----AILRYDGAAAVEPTTTQTTSTAPLNEV 324
                                                                                                                                                                                                                                                                                                                           NYTESIDGHNMTIIETDSINTA-----
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linear
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Lexington Avenue, Suite 6400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%; Score 228.5; DB 5; 22.8%; Pred. No. 1.2e-13; ative 70; Mismatches 212;
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                                                                                                                   -GWTHPIHIHLVDFKVISRTSGNNARTVMPYE 463
                                                                                                                                                                                                                                                                                                                       -----PLVVDSIQIFAAQRYSFVLE-AN 272
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                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                 Query Match 7.4%; Score 226; DB 1; Best Local Similarity 22.8%; Pred. No. 2.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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151 E----PGSFKDYYYPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSG
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                                                      101 KEKVMLVNNSIIGPTIFADWGDTIQVTVINNLETNGTSIHWHGLHQKGTNLHDG-ANGIT 159
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/4 FILING DATE: 15-MAY-1995
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                                                                                                                                                         60 QPRLTVTNPVNGQEIWY-----YEVE-----IKPFTHQVYPDLGSAD-LVGYDGMS 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United ZIP: 10174-6401
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                                                                                                                                                                                                                              3 KHTLGAAALSLLFNSNAVQASPVPETSPATGHLFKRVAQISPQYPMFTVPL---PIPPVK 59
                                                                                                                                                                                          2 KSFISAATLLVGILTPSVAAAP-----PST------PEQRDLLVPITEREEAAVK 45
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OXENB LL, Karen M.
AASLYNG, Dorrit A.
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Patent No. 5948121
GENERAL INFORMATION:
                                                                                                                              ATTORNEY_AGENT INFORMATION:

NAME: Gregg, Valeta

REGISTRATION NUMBER: 35,127

REFERENCE/DOCKET NUMBER: 4639

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123
                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 20-MAY-19
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dorric numbers H.
APPLICANT: Sorensen, Niels H.
APPLICANT: Numbers Niels H.
Laccases with Improved Dyeing
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                TYPE: am TOPOLOGY:
                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGVFPI----SDYYYSSADELVELTKNSGAPFSDNVLFNGTAKHPETGEGEYANVTLTPG 269
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New York
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                                                                                                               212-878-9655
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US-08-939-218A-2
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                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: BERKA,
                                                                                                                                APPLICANT:
            CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59812430 No.
                                                              TITLE OF INVENTION:
                                                                                                APPLICANT:
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                                                NUMBER OF SEQUENCES:
                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                   PFPGVYMFHCHNLIHEDHDMMAAFNATVLPDYGYNATVFVDPMEEL------WQARPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHGHDFYVLGRSPDESPASNERHVFDPARDAGLLSGANPVRRDVTMLPAFGWVVL-AFRA
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                                                                                                                                                                                                                                                                                                                                                 ----LGEFQAQSGQFSVQA 553
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                        XU, Feng
SCHREIDER, Palle
SCHREIDER, Palle
OXENB LL, Karen M.
AASLYNG, DORTIT A.
NVENTION: PURIFIED MYCELIOPHTHORA LACCASES
NVENTION: ACIDS ENCFODING SAME
405
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Lexington
                                                                                                                                                                 Stephen H.
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Avenue,
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Pred. No. 2.8e-13;
5981243disk of
e, 64th Floor
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                 5981243th America,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 620 amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, Carol E.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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    482
                                      440 IHLVDFKVISR----TSGNNARTVM--PYESGL-----KDVVWLGRRETVVVEAHYA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 ARQQSCNTPSN-RACWIDGYDINTDYEVDSPDIGVVRPYT----LILITEVDNWIGPDGVV 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 29-SE
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                                                                                                                                                                        CLDLPNLKPVVARDVPLSGFAKRPDNTLDVTL--DTTGTPLF-----VWKVNGSAIN 428
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LHGHDFYVLGRSPDESPASNERHVFDPARDAGLLSGANPVRRDVTMLPAFGWVVL~AFRA 540
                                                                                      IDWGRPVVDYVLTQN---TSFPPGYNIVE----VNGADQWSYWLIENDPGAPFTLPHPMH 481
                                                                                                                                                                                                                                                               RYDVVIEASRTPGNYWFNVTFGGGLLCGGSRNPYPAAIFHYAGAPGGPPTDEGKAPVDHN 378
                                                                                                                                                                                                                                                                                                      RYEVVFDFSDYAGK-----TIELRNLGGSIGGIGTD----TDYD 348
                                                                                                                                                                                                                                                                                                                                                                                          RKYRFRFLDAAVSRSFGLYFAD---TDAIDTRLPFKVIASDSGLLEHPADTSLLYISMAE 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECPIPPKGGRKVYRFKAQQYGTSWYHS---HFSAQYG-NGVVGAIQINGPA--SLPYDTD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E----PGSFKDYYYPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDALNLPSG 206
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                                                                                                                               RRHRLRLINTSVENHFQVSLVNHTMTIIAADMVPVNAMTVDS------LFLGVGQ 318
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: United States
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; MOLECULE TYPE:
US-08-462-484-8
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US-08-462-484-8
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 117; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 4185.010-US TELECOMMUNICATION INFORMATION: TELEPHONE: 212.867.0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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STREET: 405 Lexii
CITY: New York
STATE: New York
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101 AAFVNQCPIATGNSFL-YDFTATDQAGTFWYHSH-LSTQYCDGLRGPMVVYDPSDPHADL
                                   148 -----DITEPGSFKDYYYPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDA 200
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FILING DATE: 05-JUN-1995
                                                                                                                                                          15 HSFGRVS-----GDVSPDGF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 10174-6401
                                                                            43 TRAAVLANGYFPGPLITGNKGDNFQINVIDNLSNETMLKSTSIHWHGFFQKGT--NWADG 100
                                                                                                                  94 SADLVGYDGMSPGPTFQVPRGVETVVRFINNAE----APNSVHLHGSFSRAAFDGWAE- 147
                                                                                                                                                                                                34 HLFKRVAQISPQYPMFTVPLPIPPVKQPRLTVTNPVNGQEIWYYEVEIKPFTHQVYPDLG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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Query Match
Best Local Similarity
Matches 117; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: FORM: PC-DOS/MS-DOS
TYPEM: PC-DOS/MS-DOS
TYPEM: PC-DOS/MS-DOS
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TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATOREY/AGENT INFORMATION:
NAME: LOWNEY, KAZEN A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 418
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,867,0123
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CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 57704180 No. 5770418disk of No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 No. 1000 
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STATE: New York
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                         LENGTH:
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Dalboge, Henrik
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7.3%; Score 223.5;
21.7%; Pred. No. 3.56
Live 60; Mismatches
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                                                                                                                       414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
                                         452
                                                                                                                                                                                                       366 DTSVVP---ANLRDVPFPSPT-----TNTPRQFRFGRTGPTWTINGVAFADVQNRL 413
                                                                                                                                                                                                                                                  255
                                                                                                                                                                                                                                                                                       313 ERYEVVF----DESDYAGKTIELRNLGGSIGGIGTDTDYDNTDKVMRFVVA----DDTTQP 365
                                                                                                                                                                                                                                                                                                                                   210
                                                                                                                                                                                                                                                                                                                                                                            260
                                                                                                                                                                                                                                                                                                                                                                                                                   159 YDV-----DETTIITLSDWYHTAASL----GAAFPIGSDSTLINGTDLAVITVEQGKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 LNLPSGYGEFDIPMILTSKQYTANGNLVTTNGELNSFWGDVIHVNGQPWPFKNVEP-RKY
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GSTDTNFVNPVR----RDVVNTGTVGDNVTIRFTTDNPGPWFLHCHIDFHLEAGFAIVFS 480
                                                                                                                                                              TTSVLPLDEANL--VPLDSPAAPGDPNIGGVDYALNLDENEDGTNEFINDVSEVSPTVPV
                                                                                                                                                                                                                                                                                                                                                                       RFRFLDAAVSRSF-----GLYFADTDAIDTRLPFKVIASDSGLLEHPADTSLLYISMA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRAAVLANGVFPGPLITGNKGDNFQINVIDNLSNETMLKSTSIHWHGFFQKGT--NWADG
                                       SGNNARTVMPYESGLKDVVWLGRRETVVVEAHYAPFPGVYMFHCHNLIHEDHDMMAAFN 510
                                                                                                                                                                                                                                                QRYSFVLTADQDIDNYFIRALPSAGTTSFDGGINS--
                                                                                                                                                                                                                                                                                                                                   RMRLLSLSCDPNYVFSIDGHNMTIIEADAVN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SADLVGYDGMSPGPTFQVPRGVETVVRFINNAE-----APNSVHLHGSFSRAAFDGWAE- 147
                                                                                LLQILSGTTSAADLLPSGSLFAVPSNSTIEISFPITATNAPGAPHPFHLHGHTFSIVRTA 424
                                                                                                                       LANVPVGTVERWELINAGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----DITEPGSFKDYYYPNRQSARTLWYHDHAMHITAENAYRGQAGLYMLTDPAEDA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -AAIGPVTD--LTISN-
                                                                                                                     ----GWTHPIHIHLVDFKVISRT
                                                                                                                                                                                                                                                -AILRYSGASEVDPTTTE
                                                                                                                                                                                                                                                                                                                                ---HEPLTVDSIQIYAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GDVSPDGF 42
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